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(54) Title: METHOD OF DESIGNING AGONISTS AND ANTAGONISTS TO IGF RECEPTOR

(57) Abstract

The present invention relates to a method of designing compounds able to bind to a molecule of the insulin receptor family and to modulate the activity mediated by the receptor based on the 3-D structure coordinates of a IGF-1 receptor crystal of Figure 1.

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METHOD OF DESIGNING AGONISTS AND ANTAGONISTS TO IGF RECEPTOR

Field of the Invention

This invention relates to the field of receptor structure and receptor/ligand interactions. In particular it relates to the field of using receptor structure to predict the structure of related receptors and to the use of the determined structures and predicted structures to select and screen for agonists and antagonists of the polypeptide ligands.

Background of the Invention

Insulin is the peptide hormone that regulates glucose uptake and metabolism. The two types of diabetes mellitus are associated either with an inability to produce insulin because of destruction of the pancreatic islet cells (Homo-Delarche, F. & Boitard, C.,1996, Immunol. Today 10: 456-460) or with poor glucose metabolism resulting from either insulin resistance at the target tissues, or from inadequate insulin secretion by the islets or faulty liver function (Taylor, S. I., et al., 1994, Diabetes, 43: 735-740).

Insulin-like growth factors-1 and 2 (IGF-1 and 2) are structurally related to insulin, but are more important in tissue growth and development than in metabolism. They are primarily produced in the liver in response to growth hormone, but are also produced in most other tissues, where they function as paracrine/autocrine regulators. The IGFs are strong mitogens, and are involved in numerous physiological states and certain cancers (Baserga, R., 1996, TibTech 14: 150-152).

Epidermal growth factor (EGF) is a small polypeptide cytokine that is unrelated to the insulin/IGF family. It stimulates marked proliferation of epithelial tissues, and is a member of a larger family of structurally-related cytokines, such as transforming growth factor α, amphiregulin, betacellulin, heparin-binding EGF and some viral gene products. Abnormal EGF family signalling is a characteristic of certain cancers (Soler, C. & Carpenter, G., 1994 In Nicola, N. (ed) Guidebook to Cytokines and Their receptors", Oxford Univ. Press, Oxford, pp194-197; Walker, F. & Burgess, A. W., 1994, In Nicola, N. (ed) Guidebook to Cytokines and Their receptors", Oxford Univ. Press, Oxford, pp198-201).

Each of these growth factors mediates its biological actions through binding to the corresponding receptor. The IR, IGF-1R and the insulin receptor-related receptor (IRR), for which the ligand is not known, are closely related to each other, and are referred to as the insulin receptor subfamily. A

large body of information is now available concerning the primary structure of these insulin receptor subfamily members (Ebina, Y., et al., 1985 Cell 40: 747-758; Ullrich, A., et al., 1985, Nature 313: 756-761; Ullrich, A. et al., 1986, EMBO J 5: 2503-2512; Shier, P. & Watt, V. M., 1989, J. Biol. Chem. 264: 14605-14608) and the identification of some of their functional domains (for reviews see De Meyts, P. 1994, Diabetologia 37: 135-148; Lee, J. & Pilch, P. F. 1994 Amer. J. Physiol. 266: C319-C334.; Schaffer, L. 1994, Eur. J. Biochem. 221: 1127-1132). IGF-1R, IR and IRR are members of the tyrosine kinase receptor superfamily and are closely related to the epidermal growth factor receptor (EGFR) subfamily, with which they share significant sequence identity in the extracellular region as well as in the cytoplasmic kinase domains (Ullrich, A. et al., 1984 Nature 309: 418-425; Ward, C. W. et al., 1995 Proteins: Structure Function & Genetics 22: 141-153). Both the insulin and EGF receptor subfamilies have a similar arrangement of two homologous domains (L1 and L2) separated by a cys-rich region of approximately 160 amino acids containing 22-24 cys residues (Bajaj, M., et al., 1987 Biochim. Biophys. Acta 916: 220-226; Ward, C. W. et al., 1995 Proteins: Structure Function & Genetics 22: 141-153). The C-terminal portion of the IGF-1R ectodomain (residues 463 to 906) is comprised of four domains: a connecting domain, two fibronectin type 3 (Fn3) repeats, and an insert domain (O'Bryan, J. P., et al., 1991 Mol Cell Biol 11: 5016-5031). The C-terminal portion of the EGFR ectodomain (residues 477-621) consists solely of a second cys-rich region containing 20 cys residues (Ullrich, A. et al., 1984, Nature 309: 418-425).

Little is known about the secondary, tertiary and quaternary structure of the ectodomains of these receptor subfamilies. Unlike the members of the EGFR subfamily which are transmembrane monomers which dimerise on binding ligand, the IR subfamily members are homodimers, held together by disulphide bonds. The extracellular region of the IR/IGF-1R/IRR monomers contains an α-chain (~ 703 to 735 amino acid residues) and 192-196 residues of the ß-chain. There is a ~23 residue transmembrane segment, followed by the cytoplasmic portion (354 to 408 amino acids), which contains the catalytic tyrosine kinase domain flanked by juxtamembrane and C-tail regulatory regions and is responsible for mediating all receptor-specific functions (White, M. F. & Kahn, C. R. 1994 J. Biol. Chem. 269: 1-4). Chemical analyses of the receptor suggest that the α-chains are linked to the ß-chains

via a single disulphide bond, with the IR dimer being formed by at least two α-α disulphide linkages (Finn, F. M., et al., 1990, Proc. Natl. Acad. Sci. 87: 419-423; Chiacchia, K. B., 1991, Biochem. Biophys. Res. Commun. 176, 1178-1182; Schaffer, L. & Ljungqvist, L., 1992, Biochem. Biophys. Res. Comm. 189: 650-653; Sparrow, L. G., et al., 1997, J. Biol. Chem. 47: 29460-29467).

Although the three-dimensional (3D) structures of the ligands EGF, TGF-alpha (Hommel, U., et al., 1992, J. Mol. Biol. 227:271-282), insulin (Dodson, E. J., et al., 1983, Biopolymers 22:281-291), IGF-1 (Sato, A., et al., 1993, Int J Peptide Protein Res 41:433-440) and IGF-2 (Torres, A. M., et al.,1995, J. Mol. Biol. 248:385-401) are known, and numerous analytical and functional studies of ligand binding to EGFR (Soler, C. & Carpenter, G., 1994 In Nicola (ed) Guidebook to Cytokines and Their receptors", Oxford Univ. Press, Oxford, pp194-197), IGF-1R and IR (see De Meyts, P., 1994 Diabetologia, 37:135-148) have been carried out, the mechanisms of ligand binding and subsequent transmembrane signalling have not been resolved.

Ligand-induced, receptor-mediated phosphorylation is the signalling mechanism by which most cytokines, polypeptide hormones and membrane-anchored ligands exert their biological effects. The primary kinase may be part of the intracellular portion of the transmembrane receptor protein, as in the tyrosine kinase receptors (for review see Yarden, Y., et al., 1988, Ann. Rev. Biochem. 57:443-478) or the Ser/Thr kinase receptors (Alevizopoulos, A. & Mermod, N., 1997, BioEssays, 19:581-591) or may be non-covalently associated with the cytoplasmic tail of the transmembrane protein(s) making up the receptor complex, as in the case of the haemopoietic growth factor receptors (Stahl, N., et al., 1995, Science 267:1349-1353). The end result is the same, ligand binding leads to receptor dimerization or oligomerization or a conformational change in pre-existing receptor dimers or oligomers, resulting in activation by transphosphorylation, of the covalently attached or non-covalently associated protein kinase domains (Hunter, T., 1995, Cell, 80:225-236).

Many oncogenes have been shown to be homologous to growth factors, growth factor receptors or molecules in the signal transduction pathways (Baserga, R.,1994 Cell, 79:927-930; Hunter, T., 1997 Cell, 88:333-346). One of the best examples is v-Erb (related to the EGFR). Since overexpression of a number of growth factor receptors results in ligand-dependent transformation, an alternate strategy for oncogenes is to regulate

the expression of growth factor receptors or their ligands or to directly bind to the receptors to stimulate the same effect (Baserga, R., 1994 Cell, 79:927-930). Examples are v-Src, which activates IGF-1 R intracellularly; c-Myb, which transforms cells by enhancing the expression of IGF1R; and SV40 T antigen which interacts with the IGF-1R and enhances the secretion of IGF-1 (see Baserga, R.,1994 Cell, 79:927-930 for review). Cells in which the IGF-1R has been disrupted or deleted cannot be transformed by SV40 T antigen. If oncogenes activate growth factors and their receptors, then tumour suppressor genes should have the opposite effect. One good example of this is the Wilm's tumour suppressor gene, WT1, which suppresses the expression of IGF-1R (Drummond, J. A., et al., 1992, Science, 257:275-277). Cells that are driven to proliferate by oncogenes undergo massive apoptosis when growth factor receptors are ablated, since, unlike normal cells, they appear unable to withdraw from the cell-cycle and enter into the G_0 phase (Baserga, R.,1994 Cell, 79:927-930).

The insulin-like growth factor-1 receptor (IGF-1R) is one of several growth-factor receptors that regulate the proliferation of mammalian cells. However, its ubiquitousness and certain unique aspects of its function make IGF-1R an ideal target for specific therapeutic interventions against abnormal growth, with very little effect on normal cells (see Baserga, R., 1996 TIBTECH, 14:150-152). The receptor is activated by IGF1, IGF2 and insulin, and plays a major role in cellular proliferation in at least three ways: it is essential for optimal growth of cells *in vitro* and *in vivo*; several cell types require IGF-1R to maintain the transformed state; and activated IGF-1R has a protective effect against apoptotic cell death (Baserga, R., 1996 TIBTECH, 14:150-152). These properties alone make it an ideal target for therapeutic interventions. Transgenic experiments have shown that IGF-1R is not an absolute requirement for cell growth, but is essential for the establishment of the transformed state (Baserga, R.,1994 Cell, 79: 927-930). In several cases (human glioblastoma, human melanoma; human breast carcinoma; human lung carcinoma; human ovarian carcinoma; human rhabdomyosarcoma; mouse melanoma, mouse leukaemia; rat glioblastoma; rat rhabdomyosarcoma; hamster mesothelioma) the transformed phenotype can be reversed by decreasing the expression of IGF-1R using antisense to IGF-1R (Baserga, R., 1996 TIBTECH 14:150-152); or by interfering with its function by antibodies to IGF-1R (human breast carcinoma; human

rhabdomyosarcoma) or by dominant negatives of IGF-1R (rat glioblastoma; Baserga, R.,1996 TIBTECH 14:150-152).

Three effects are observed when the function of IGF-1R is impaired: tumour cells undergo massive apoptosis which results in inhibition of tumourogenesis; surviving tumour cells are eliminated by a specific immune response; and such a host response can cause a regression of an established wild-type tumour (Resnicoff, M., et al., 1995, Cancer Res. 54:2218-2222). These effects, plus the fact that interference with IGF-1R function has a limited effect on normal cells (partial inhibition of growth without apoptosis) makes IGF-1R a unique target for therapeutic interventions (Baserga, R., 1996 TIBTECH 14:150-152). In addition IGF-1R is downstream of many other growth factor receptors, which makes it an even more generalised target. The implication of these findings is that if the number of IGF-1Rs on cells can be decreased or their function antagonised, then tumours cease to grow and can be removed immunologically. These studies establish that IGF-1R antagonists will be extremely important therapeutically.

Many cancer cells have constitutively active EGFR (Sandgreen, E. P., et al., 1990, Cell, 61:1121-135; Karnes, W. E. J., et al., 1992, Gastroenterology, 102:474-485) or other EGFR family members (Hines, N. E.,1993, Semin. Cancer Biol. 4:19-26). Elevated levels of activated EGFR occur in bladder, breast, lung and brain tumours (Harris, A. L., et al., 1989, In Furth & Greaves (eds) The Molecular Diagnostics of human cancer. Cold Spring Harbor Lab. Press, CSH, NY, pp353-357). Antibodies to EGFR can inhibit ligand activation of EGFR (Sato, J. D., et al., 1983 Mol. Biol. Med. 1:511-529) and the growth of many epithelial cell lines (Aboud-Pirak E., et al., 1988, J. Natl Cancer Inst. 85:1327-1331). Patients receiving repeated doses of a humanised chimeric anti-EGFR monoclonal antibody showed signs of disease stabilization. The large doses required and the cost of production of humanised monoclonal antibody is likely to limit the application of this type of therapy. These findings indicate that the development of EGF antagonists will be attractive anticancer agents.

Summary of the Invention

The present inventors have now obtained 3D structural information concerning the insulin-like growth factor receptor (IGF-1R). This information can be used to predict the structure of related members of the insulin

receptor family and provides a rational basis for the development of ligands for specific therapeutic applications.

Accordingly, in a first aspect the present invention provides a method of designing a compound able to bind to a molecule of the insulin receptor family and to modulate an activity mediated by the molecule, including the step of assessing the stereochemical complementarity between the compound and the receptor site of the molecule, wherein the receptor site includes:

(a) amino acids 1 to 462 of the receptor for IGF-1, having the atomic coordinates substantially as shown in Figure 1;

(b) a subset of said amino acids, or;

(c) amino acids present in the amino acid sequence of a member of the insulin receptor family, which form an equivalent three-dimensional structure to that of the receptor molecule as depicted in Figure 1.

The phrase "insulin receptor family" encompasses, for example, IGF-1R, IR and IRR. In general, insulin receptor family members show similar domain arrangements and share significant sequence identity (preferably at least 40% identity).

By "stereochemical complementarity" we mean that the biologically active substance or a portion thereof correlates, in the manner of the classic "lock-and-key" visualisation of ligand-receptor interaction, with the groove in the receptor site.

In a preferred embodiment of this aspect of the invention, the compound is selected or modified from a known compound identified from a database.

In a further preferred embodiment, the compound is designed so as to complement the structure of the receptor molecule as depicted in Figure 1.

In a further preferred embodiment, the compound has structural regions able to make close contact with amino acid residues at the surface of the receptor site lining the groove, as depicted in Figure 2.

In a further preferred embodiment, the compound has a stereochemistry such that it can interact with both the L1 and L2 domains of the receptor site.

In a further preferred embodiment, the compound has a stereochemistry such that it can interact with the L1 domain of a first monomer of the receptor homodimer, and with the L2 domain of the other monomer of the receptor homodimer.

In a further preferred embodiment, the interaction of the compound with the receptor site alters the position of at least one of the L1, L2 or cysteine-

rich domains of the receptor molecule relative to the position of at least one of the other of said domains. Preferably, the compound interacts with the β sheet of the L1 domain of the receptor molecule, thereby causing an alteration in the position of the L1 domain relative to the position of the cysteine-rich domain or of the L2 domain. Alternatively, the compound interacts with the receptor site in the region of the interface between the L1 domain an the cysteine-rich domain of the receptor molecule, thereby causing the L1 domain and the cysteine-rich domain to move away from each other. In another preferred embodiment, the compound interacts with the hinge region between the L2 domain and the cysteine-rich domain of the receptor molecule, thereby causing an alteration in the positions of the L2 domain and the cysteine-rich domain relative to each other.

In a further preferred embodiment, the stereochemical complementarity between the compound and the receptor site is such that the compound has a K_b for the receptor side of less than 10^{-6}M, more preferably is less than 10^{-8}M.

In a further preferred embodiment or the first aspect of the present invention, the compound has the ability to increase an activity mediated by the receptor molecule.

In a further preferred embodiment, the compound has the ability to decrease an activity mediated by the receptor molecule. Preferably, the stereochemical interaction between the compound and the receptor site is adapted to prevent the binding of a natural ligand of the receptor molecule to the receptor site. It is preferred that the compound has a K_i of less than 10^{-6}M, more preferably less than 10^{-8}M and more preferably less than 10^{-9}M.

In a further preferred embodiment of the first aspect of the present invention, the receptor is the IGF-1R, or the insulin receptor.

In a second aspect, the present invention provides a computer-assisted method for identifying potential compounds able to bind to a molecule of the insulin receptor family and to modulate an activity mediated by the molecule, using a programmed computer including a processor, an input device, and an output device, including the steps of:

(a) inputting into the programmed computer, through the input device, data comprising the atomic coordinates of the IGF-1R molecule as shown in Figure 1, or a subset thereof;

(b) generating, using computer methods, a set of atomic coordinates of a structure that possesses stereochemical complementarity to the atomic

coordinates of the IGF-1R site as shown in Figure 1, or a subset thereof, thereby generating a criteria data set;

(c) comparing, using the processor, the criteria data set to a computer database of chemical structures;

(d) selecting from the database, using computer methods, chemical structures which are structurally similar to a portion of said criteria data set; and

(e) outputting, to the output device, the selected chemical structures which are similar to a portion of the criteria data set.

In a preferred embodiment of the second aspect, the programmed computer includes a data storage system which includes the dtatbase of chemical structures.

In a preferred embodiment of the second aspect, the method is used to identify potential compounds which have the ability to decrease an activity mediated by the receptor.

In another preferred embodiment, the computer-assisted method further includes the step of selecting one or more chemical structures from step (e) which interact with the receptor site of the molecule in a manner which prevents the binding of natural ligands to the receptor site.

In another preferred embodiment, the computer-assisted method further includes the step of obtaining a compound with a chemical structure selected in steps (d) and (e), and testing the compound for the ability to decrease an activity mediated by the receptor.

In a further preferred embodiment, the computer-assisted method is used to identify potential compounds which have the ability to increase an activity mediated by the receptor molecule.

In another preferred embodiment, the computer-assisted method further includes the step of obtaining a molecule with a chemical structure selected in steps (d) and (e), and testing the compound for the ability to increase an activity mediated by the receptor.

In a further preferred embodiment of the second aspect of the present invention, the receptor is the IGF-1R, or the insulin receptor.

In a third aspect, the present invention provides a method of screening of a putative compound having the ability to modulate the activity of a receptor of the insulin receptor family, including the steps of identifying a putative compound by a method according to the first or second aspects, and testing the

compound for the ability to increase or decrease an activity mediated by the receptor.

In a preferred embodiment of the third aspect, the test is carried out *in vitro*.

In a further preferred embodiment of the third aspect, the test is a high throughput assay.

In a preferred embodiment of the third aspect, the test is carried out *in vivo*.

Brief Description of the Drawings

Figure 1. IGF-1R residues 1-462, in terms of atomic coordinates refined to a resolution of 2.6 Å (average accuracy ≈ 0.3Å). The coordinates are in relation to a Cartesian system of orthogonal axes.

Figure 2. Depiction of the residues lining the groove of the IGF-1R receptor fragment 1-462.

Figure 3. Gel filtration chromatography of affinity-purified IGF-1R/462 protein. The protein was purified on a Superdex S200 column (Pharmacia) fitted to a BioLogic L.C. system (Biorad), equilibrated and eluted at 0.8 ml/min with 40 mM Tris/150 mM NaCl/0.02% NaN3 adjusted to pH 8.0. (a) Protein eluting in peak 1 contained aggregated IGF-1R/462 protein, peak 2 contained monomeric protein and peak 3 contained the c-myc undecapeptide used for elution from the Mab 9E10 immunoaffinity column. (b) Non-reduced SDS-PAGE of fraction 2 from IGF-1R/462 obtained following Superdex S200 (Fig.1a). Standard proteins are indicated.

Figure 4. Ion exchange chromatography of affinity-purified, truncated IGF-1R ectodomain. A mixture of gradient and isocratic elution chromatography was performed on a Resource Q column (Pharmacia) fitted to a BioLogic System (Biorad), using 20 mM Tris/pH 8.0 as buffer A and the same buffer containing 1M NaCl as buffer B. Protein solution in TBSA was diluted at least 1:2 with water and loaded onto the column at 2 ml/min. Elution was monitored by absorbance (280 nm) and conductivity (mS/cm). Target protein (peak 2) eluted isocratically with 20 mM Tris/0.14 M NaCl pH 8.0. Inset:

Isoelectric focusing gel (pH 3 - 7; Novex Australia Pty Ltd)of fraction 2. The pI was estimated at 5.1 from standard proteins (not shown).

Figure 5. Polypeptide fold for residues 1-462 of IGF-1R. The L1 domain is at the top, viewed from the N-terminal end and L2 is at the bottom. The space at the centre is of sufficient size to accommodate IGF-1. Helices are indicated by curled ribbon and b-strands by arrows. Cysteine side chains are drawn as ball-and-stick with lines showing disulfide bonds. The arrow points in the direction of view for L1 in Figure 7.

Figure 6. Amino acid sequences of IGF-1R and related proteins. a, L1 and L2 domains of human IGF-1R and IR are shown based on a sequence alignment for the two proteins and a structural alignment for the L1 and L2domains. Positions showing conservation physico-chemical properties of amino acids are boxed, residues used in the structural alignment are shown in Times Italic and residues which form the Trp 176 pocket are in Times Bold. Secondary structure elements for L1 (above the sequences) and L2 (below) are indicated as cylinders for helices and arrows for β-strands. Strands are shaded (pale, medium and dark grey) according to the β-sheet to which they belong. Disulfide bonds are also indicated. b, Cys-rich domains of human IGF-1R, IR and EGFR (domains 2 and 4) are aligned based on sequence and structural considerations. Secondary structural elements and disulfide bonds are indicated above the sequences. The dashed bond is only present in IR. Different types of disulfide bonded modules are labelled below the sequences as open, filled or broken lines. Boxed residues show conservation of physico-chemical properties and structurally conserved residues for modules 4-7 are shown in Times Italic. Residues from EGFR which do not conform to the pattern are in lowercase with probable disulfide bonding indicated below and the conserved Trp 176 and the semi-conserved Gln 182 are in Times Bold.

Figure 7. Stereo view of a superposition of the L1 (white) and L2 (black) domains. Residues numbers above are for L1 and below for L2. The side chain of Trp 176 which protrudes into the core of L1 is drawn as ball-and-stick.

Figure 8. Schematic diagram showing the association of three β-finger motifs. β-strands are drawn as arrows and disulfide bonds as zigzags.

Figure 9: Sequence alignment of hIGF-1R, hIR and hIRR ectodomains, derived by use of the PileUp program in the software package of the Genetics Computer Group, 575 Science Drive, Madison, Wisconsin, USA. For assignment of homologous 3D structures see Figure 6.

Figure 10 Gel filtration chromatography of insulin receptor ectodomain and MFab complexes. hIR -11 ectodomain dimer (5 - 20 mg) was complexed with MFab derivatives (15-25 mg each) of the anti-hIR antibodies 18-44, 83-7 and 83-14 (Soos et al., 1986). Flution profiles were generated from samples loaded on to a Superdex S200 column (Pharmacia), connected to a BioLogic chromatography system (Biorad) and monitored at 280 nm. The column was eluted at 0.8 ml/min with 40 mM Tris/150 mM sodium chloride/0.02% sodium azide buffer adjusted to pH 8.0: Profile 0, hIR -11 ectodomain, Profile 1, ectodomain mixed with MFab 18-44; Profile 2 , ectodomain mixed with MFab18-44 and MFab 83-14; Profile 3, ectodomain mixed with MFab 18-44, MFab 83-14 and MFab 83-7. The apparent mass of each complex was determined from a plot of the following standard proteins: thyroglobulin (660 kDa), ferritin (440 kDa), bovine gamma globulin (158 kDa), bovine serum albumin (67 kDa), chicken ovalbumin (44 kDa) and equine myoglobin (17 kDa).

Figure 11 Schematic representations of electron microscopy images of the hIR ectodomain dimer.

Detailed Description of the Invention

We describe herein the expression, purification, and crystallization of a recombinant truncated IGF-1R fragment (residues 1-462) containing the L1-cysteine-rich-L2 region of the ectodomain. The selected truncation position is just downstream of the exon 6/exon 7 junction (Abbott, A. M., et al., 1992. J Biol Chem., 267:10759-10763), and occurs at a position where the sequences of the IR and EGFR families diverge markedly (Ward, C. W., et al.,1995, Proteins: Struct., Funct., Genet. 22:141-153; Lax, I., et al., 1988, Molec. Cellul. Biol. 8:1970-1978) suggesting it represents a domain boundary. To

limit the effects of glycosylation, the IGF-1R fragment was expressed in Lec8 cells, a glycosylation mutant of Chinese hamster ovary (CHO) cells, whose defined glycosylation defect produces N-linked oligosaccharides truncated at N-acetyl glucosamine residues distal to mannose residues (Stanley, P. 1989, Molec. Cellul. Biol. 9:377-383). Such an approach has facilitated glycoprotein crystallization (Davis, S. J., et al., 1993, Protein Eng. 6:229-232; Liu, J., et al., 1996, J. Biol. Chem. 271:33639-33646).

The IGF-1R construct described herein includes a c-myc peptide tag (Hoogenboom, H. R., et al.,1991, Nucleic Acids Res. 19:4133-4137) that is recognised by the Mab 9E10 (Evan, G. I., et al., 1985, Mol. Cell. Biol. 5:3610-3616) enabling the expressed product to be purified by peptide elution from an antibody affinity column followed by gel filtration over Superdex S200. The purified proteins crystallized under a sparse matrix screen (Jancarik, J. & Kim, S.-H., 1991, J. Appl. Cryst. 24:409-411) but the crystals were of variable quality, with the best diffracting to 3.0-3.5Å. Isocratic gradient elution by anion-exchange chromatography yielded protein that was less heterogenous and gave crystals of sufficient quality to determine the structure of the first three domains of the human IGF-1R.

The IGF-1R fragment consisted of residues 1-462 of IGF-1R linked via an enterokinase-cleavable pentapeptide sequence to an eleven residue c-myc peptide tag at the C-terminal end. The fragment was expressed in Lec8 cells by continuous media perfusion in a bioreactor using porous carrier disks. It was secreted into the culture medium and purified by peptide elution from an anti-c-myc antibody column followed by Superdex S200 gel filtration. The receptor fragment bound two anti-IGF-1R monoclonal antibodies, 24-31 and 24-60, which recognize conformational epitopes, but could not be shown to bind IGF-1 or IGF-2. Crystals of variable quality were grown as rhombic prisms in 1.7 M ammonium sulfate at pH 7.5 with the best diffracting to 3.0-3.5 Å. Further purification by isocratic elution on an anion-exchange column gave protein which produced better quality crystals, diffracting to 2.6 Å, that were suitable for X-ray structure determination.

The structure of this fragment (IGF-1R residues 1-462; L1-cys rich-L2 domains) has been determined to 2.6 Å resolution by X-ray diffraction. The L domains each adopt a compact shape consisting of a single stranded right-handed β-helix. The cys-rich region is composed of eight disulphide-bonded modules, seven of which form a rod-shaped domain with modules associated

in a novel manner. At the centre of this reasonably extended structure is a space, bounded by all three domains, and of sufficient size to accommodate a ligand molecule. Functional studies on IGF-1R and other members of the insulin receptor family show that the regions primarily responsible for hormone-binding map to this central site. Thus this structure gives a first view of how members of the insulin receptor family might interact with their ligands.

Another group has reported the crystallization of a related receptor, the EGFR, in a complex with its ligand EGF (Weber, W., et al., 1994, J Chromat. 679:181-189). However, difficulties were encountered with these crystals which diffracted to only 6 Å, insufficient for the determination of an atomic resolution structure of this complex (Weber, W., et al., 1994, J Chromat 679:181-189) or the generation of accurate models of structurally related receptor domains such as IGF-1R and IR by homology modelling.

The present inventors have developed 3D structural information about cytokine receptors in order to enable a more accurate understanding of how the binding of ligand leads to signal transduction. Such information provides a rational basis for the development of ligands for specific therapeutic applications, something that heretofore could not have been predicted *de novo* from available sequence data.

The precise mechanisms underlying the binding of agonists and antagonists to the IGF-1R site are not fully clarified. However, the binding of ligands to the receptor site, preferably with an affinity in the order of 10^{-8}M or higher, is understood to arise from enhanced stereochemical complementarity relative to naturally occurring IGF-1 ligands.

Such stereochemical complementarity, pursuant to the present invention, is characteristic of a molecule that matches intra-site surface residues lining the groove of the receptor site as eneumerated by the coordinates set out in Figure 1. The residues lining the groove are depicted in Figure 2. By "match" we mean that the identified portions interact with the surface residues, for example, via hydrogen bonding or by enthalpy-reducing Van der Waals interactions which promote desolvation of the biologically active substance within the site, in such a way that retention of the biologically active substance within the groove is favoured energetically.

Substances which are complemetary to the shape of the receptor site characterised by amino acids positioned at atomic coordinates set out in

Figure 1 may be able to bind to the receptor site and, when the binding is sufficiently strong, substantially prohibit binding of the naturally occurring ligands to the site.

It will be appreciated that it is not necessary that the complementarity between ligands and the receptor site extend over all residues lining the groove in order to inhibit binding of the natural ligand. Accordingly, agonists or antagonists which bind to a portion of the residues lining the groove are encompassed by the present invention.

In general, the design of a molecule possessing stereochemical complementarity can be accomplished by means of techniques that optimize, either chemically or geometrically, the "fit" between a molecule and a target receptor. Known techniques of this sort are reviewed by Sheridan and Venkataraghavan, Acc. Chem Res. 1987 20 322; Goodford, J. Med. Chem. 1984 27 557; Beddell, Chem. Soc. Reviews 1985, 279; Hol, Angew. Chem. 1986 25 767 and Verlinde C.L.M.J & Hol, W.G.J. Structure 1994, 2, 577, the respective contents of which are hereby incorporated by reference. See also Blundell et al., Nature 1987 326 347 (drug development based on information regarding receptor structure).

Thus, there are two preferred approaches to designing a molecule, according to the present invention, that complements the shape of IGF-1R or a related receptor molecule. By the geometric approach, the number of internal degrees of freedom (and the corresponding local minima in the molecular conformation space) is reduced by considering only the geometric (hard-sphere) interactions of two rigid bodies, where one body (the active site) contains "pockets" or "grooves" that form binding sites for the second body (the complementing molecule, as ligand). The second preferred approach entails an assessment of the interaction of respective chemical groups ("probes") with the active site at sample positions within and around the site, resulting in an array of energy values from which three-dimensional contour surfaces at selected energy levels can be generated.

The geometric approach is illustrated by Kuntz et al., J. Mol. Biol. 1982 161 269, the contents of which are hereby incorporated by reference, whose algorithm for ligand design is implemented in a commercial software package distributed by the Regents of the University of California and further described in a document, provided by the distributor, which is entitled "Overview of the DOCK Package, Version 1.0,", the contents of which are

hereby incorporated by reference. Pursuant to the Kuntz algorithm, the shape of the cavity represented by the IGF-R1 site is defined as a series of overlapping spheres of different radii. One or more extant data bases of crystallographic data, such as the Cambridge Structural Database System maintained by Cambridge University (University Chemical Laboratory, Lensfield Road, Cambridge CB2 1EW, U.K.) and the Protein Data Bank maintained by Brookhaven National Laboratory (Chemistry Dept. Upton, NY 11973, U.S.A.), is then searched for molecules which approximate the shape thus defined.

Molecules identified in this way, on the basis of geometric parameters, can then be modified to satisfy criteria associated with chemical complementarity, such as hydrogen bonding, ionic interactions and Van der Waals interactions.

The chemical-probe approach to ligand design is described, for example, by Goodford, J. Med. Chem. 1985 28 849, the contents of which are hereby incorporated by reference, and is implemented in several commercial software packages, such as GRID (product of Molecular Discovery Ltd., West Way House, Elms Parade, Oxford OX2 9LL, U.K.). Pursuant to this approach, the chemical prerequisites for a site-complementing molecule are identified at the outset, by probing the active site (as represented via the atomic coordinates shown in Fig. 1) with different chemical probes, e.g., water, a methyl group, an amine nitrogen, a carboxyl oxygen, and a hydroxyl. Favored sites for interaction between the active site and each probe are thus determined, and from the resulting three-dimensional pattern of such sites a putative complementary molecule can be generated.

The chemical-probe approach is especially useful in defining variants of a molecule known to bind the target receptor. Accordingly, crystallographic analysis of IGF-1 bound to the receptor site is expected to provide useful information regarding the interaction between the archetype ligand and the active site of interest.

Programs suitable for searching three-dimensional databases to identify molecules bearing a desired pharmacophore include: MACCS-3D and ISIS/3D (Molecular Design Ltd., San Leandro, CA), ChemDBS-3D (Chemical Design Ltd., Oxford, U.K.), and Sybyl/3DB Unity (Tripos Associates, St. Louis, MO).

Programs suitable for pharmacophore selection and design include: DISCO (Abbott Laboratories, Abbott Park, IL), Catalyst (Bio-CAD Corp., Mountain View, CA), and ChemDBS-3D (Chemical Design Ltd., Oxford, U.K.).

Databases of chemical structures are available from a number of sources including Cambridge Crystallographic Data Centre (Cambridge, U.K.) and Chemical Abstracts Service (Columbus, OH).

De novo design programs include Ludi (Biosym Technologies Inc., San Diego, CA), Sybyl (Tripos Associates) and Aladdin (Daylight Chemical Information Systems, Irvine, CA).

Those skilled in the art will recognize that the design of a mimetic may require slight structural alteration or adjustment of a chemical structure designed or identified using the methods of the invention.

The invention may be implemented in hardware or software, or a combination of both. However, preferably, the invention is implemented in computer programs executing on programmable computers each comprising a processor, a data storage system (including volatile and non-volatile memory and/or storage elements), at least one input device, and at least one output device. Program code is applied to input data to perform the functions described above and generate output information. The output information is applied to one or more output devices, in known fashion. The computer may be, for example, a personal computer, microcomputer, or workstation of conventional design.

Each program is preferably implemented in a high level procedural or object-oriented programming language to communicate with a computer system. However, the programs can be implemented in assembly or machine language, if desired. In any case, the language may be compiled or interpreted language.

Each such computer program is preferably stored on a storage medium or device (e.g., ROM or magnetic diskette) readable by a general or special purpose programmable computer, for configuring and operating the computer when the storage media or device is read by the computer to perform the procedures described herein. The inventive system may also be considered to be implemented as a computer-readable storage medium, configured with a computer program, where the storage medium so

configured causes a computer to operate in a specific and predefined manner to perform the functions described herein.

Compounds designed according to the methods of the present invention may be assessed by a number of *in vitro* and *in vivo* assays of hormone function. For example, the identification of IGF-1R antagonists of may be undertaken using a solid-phase receptor binding assay. Potential antagonists may be screened for their ability to inhibit the binding of europium-labelled IGF ligands to soluble, recombinant IGF-1R in a microplate-based format. Europium is a lanthanide fluorophore, the presence of which can be measured using time-resolved fluorometry. The sensitivity of this assay matches that achieved by radioisotopes, measurement is rapid and is performed in a microplate format to allow high-sample throughput, and the approach is gaining wide acceptance as the method of choice in the development of screens for receptor agonists/antagonists (see Apell et.al. J. Biomolec. Screening 3:19-27, 1998 : Inglese et. al. Biochemistry 37:2372-2377, 1998).

Binding affinity and inhibitor potency may be measured for candidate inhibitors using biosensor technology.

The IGF-1R antagonists may be tested for their ability to modulate receptor activity using a cell-based assay incorporating a stably transfected, IGF-1-responsive reporter gene [Souriau, C., Fort, P., Roux, P., Hartley, O., LeFranc, M-P. and Weill, M., 1997, Nucleic Acids Res. 25, 1585-1590]. An IGF-1-responsive, luciferase reporter gene has been assembled and transfected in 293 cells. The assay addresses the ability of IGF-1 to activate the reporter gene in the presence of novel ligands. It offers a rapid (results within 6-8 hours of hormone exposure), high-throughput (assay can be conducted in a 96-well format for automated counting) analysis using an extremely sensitive detection system (chemiluminescence). Once candidate compounds have been identified, their ability to antagonise signal transduction via the IGF-1R can be assessed using a number of routine *in vitro* cellular assays such as inhibition of IGF-1-mediated cell proliferation, induction of apoptosis in the presence of IGF-1 and the ablation of IGF-1-driven anchorage-independent cell growth in soft agar [D'Ambrosio, C., Ferber, A., Resnicoff, M. and Baserga, R., 1996, Cancer Res. 56, 4013-4020]. Such assays may be conducted on the P6 cell line, a cell line highly responsive to IGF as a result of the constitutive overexpression of the IGF-1R

(45-50,000 receptors/cell, [Pietrzkowski, Z., Sell, C., Lammers, R., Ullrich, A. and Baserga, R.,1992, Cell Growth.Diff. 3, 199-205]). Ultimately, the efficacy of any antagonist as a tumour therapeutic may be tested *in vivo* in animals bearing tumour isografts and xenografts as described [Resnicoff. M., Burgaud, J-L., Rotman, H. L., Abraham, D. and Baserga, R., 1995, Cancer Res. 55, 3739-3741; Resnicoff, M., Sell, C., Rubini, M., Coppola, D., Ambrose, D., Baserga, R. and Rubin, R., 1994 Cancer Res. 54: 2218-2222].

Tumour growth inhibition assays may be designed around a nude mouse xenograft model using a range of cell lines. The effects of the receptor antagonists and inhibitors may be tested on the growth of subcutaneous tumours.

A further use of the structure of the IGF-1R fragment described here is in facilitating structure determination of a related protein, such as a larger fragment of this receptor, another member of the insulin receptor family or a member of the EGF receptor family. This new structure may be either of the protein alone, or in complex with its ligand. For crystallographic analysis this is achieved using the method of molecular replacement (Brunger, Meth. Enzym. 1997 276 558-580, Navaza and Saludjian, *ibid.* 581-594, Tong and Rossmann, *ibid.* 594-611, Bentley, *ibid.* 611-619) in a program such as XPLOR. In this procedure diffraction data is collected from a crystalline protein of unknown structure. A transform of these data (Patterson function) is compared with a Patterson function calculated from a known structure. Firstly, the one Patterson function is rotated on the other to determine the correct orientation of the unknown molecule in the crystal. The translation function is then calculated to determine the location of the molecule with respect to the crystal axes. Once the molecule has been correctly positioned in the unit cell initial phases for the experimental data may be calculated. These phases are necessary for calculation of an electron density map from which structural differences may be observed and for refinement of the structure. Due to limitations in the method the search molecule must be structurally related to that which is to be determined. However it is sufficient for only part of the unknown structure (e.g. < 50%) to be similar to the search molecule. Thus the three dimensional structure of IGF-1R residues 1-462 may be used to solve structures consisting of related receptors, enabling a program of drug design as outlined above.

In summary, the general principles of receptor-based drug design can be applied by persons skilled in the art, using the crystallographic results presented above, to produce ligands of IGF-1R or other related receptors, having sufficient stereochemical complementarity to exhibit high affinity binding to the receptor site.

The present invention is further described below with reference to the following, non-limiting examples.

EXAMPLE 1

Expression, Purification and Crystallization of the IGF-1R Fragment.

Several factors hamper macromolecular crystallization including sample selection, purity, stability, solubility (McPherson, A., et al., 1995, Structure 3:759-768); Gilliland, G. L., & Ladner, J. E., 1996, Curr. Opin. Struct. Biol. 6:595-603), and the nature and extent of glycosylation (Davis, S. J., et al., 1993, Protein Eng. 6:229-232). Initial attempts to obtain structural data from soluble IGF-1R ectodomain (residues 1-906) protein, expressed in Lec8 cells (Stanley, P. 1989, Molec. Cellul. Biol. 9:377-383) and purified by affinity chromatography, produced large, well-formed crystals (1.0 mm x 0.2 mm x 0.2 mm) which gave no discernible X-ray diffraction pattern (unpublished data). Similar difficulties have been encountered with crystals of the structurally-related epidermal growth factor receptor (EGFR) ectodomain, which diffracted to only 6 Å, insufficient for the determination of an atomic resolution structure (Weber, W. et al., 1994, J Chromat 679:181-189). This prompted us to search for a fragment of IGF-1R that was more amenable to X-ray crystallographic studies.

The fragment expressed (residues 1-462) comprises the L1-cysteine-rich-L2 region of the ectodomain. The selected truncation position at Val462 is four residues downstream of the exon 6/exon 7 junction (Abbott, A. M., et al., 1992, J Biol Chem. 267:10759-10763), and occurs at a position where the sequences of the IR and the structurally related EGFR families diverge markedly (Lax, I., et al., 1988, Molec Cell Biol. 8:1970-1978; Ward, C. W., et al., 1995, Proteins: Struct., Funct., Genet. 22:141-153), suggesting that it represents a domain boundary. The expression strategy included use of the pEE14 vector (Bebbington, C. R. & Hentschel, C. C. G., 1987, In: Glover, D. M., ed. DNA Cloning. Academic Press, San Diego. Vol 3, p163) in glycosidase-defective Lec8 cells (Stanley, P., 1989, Molec. Cellul. Biol. 9:377-

383), which produce N-linked oligosaccharides lacking the terminal galactose and N-acetylneuraminic acid residues (Davis, S. J., et al., 1993, Protein Eng. 6:229-232; Liu, T., et al., 1996, J Biol Chem 271:33639-33646.). The construct contained a C-terminal c-myc affinity tag (Hoogenboom, H. R., et al., 1991, Nucl Acids Res. 19:4133-4137), which facilitated immunoaffinity purification by specific peptide elution and avoided aggressive purification conditions. These procedures yielded protein which readily crystallized after a further gel filtration purification step. This provided a general protocol to enhance crystallisation prospects for labile, multidomain glycoproteins.

The structure of this fragment is of considerable interest, since it contains the major determinants governing insulin and IGF-1 binding specificity (Gustafson, T. A. & Rutter, W. J., 1990, J. Biol. Chem. 265:18663-18667; Andersen, A. S., et al., 1990, Biochemistry, 29:7363-7366; Schumacher, R., et al., 1991, J. Biol. Chem. 266:19288-19295; Schumacher, R., et al., 1993, J. Biol. Chem. 268:1087-1094; Schäffer, L., et al., 1993, J. Biol. Chem. 268:3044-3047; Williams, P. F., et al., 1995, , J. Biol. Chem. 270:3012-3016), and is very similar to an IGF-1R fragment (residues 1-486) reported to act as a strong dominant negative for several growth functions and which induces apoptosis of tumour cells *in vivo* (D'Ambrosio, C., et al., 1996, Cancer Res. 56:4013-4020).

The expression plasmid pEE14/IGF-1R/462 was constructed by inserting the oligonucleotide cassette:

AatII

5' GACGTC GACGATGACGATAAG GAACAAAAACTCATC

D V D D D D K E Q K L I

(EK cleavage) (c-myc tail)

S E E D L N (Stop)

TCAGAAGAGGATCTGAAT TAGAATTC GACGTC 3'

EcoRI *AatII*

encoding an enterokinase cleavage site, c-myc epitope tag (Hoogenboom, H. R., et al., 1991, Nucleic acids Res. 19:4133-4137) and stop codon into the AatII site (within codon 462) of Igf-1r cDNA in the mammalian expression vector pECE (Ebina, Y., et al., 1985, Cell, 40:747-758; kindly supplied by W. J. Rutter, UCSF, USA), and introducing the DNA comprising the 5' 1521 bp of

the cDNA (Ullrich, A., et al., 1986, EMBO J. 5:2503-2512) ligated to the oligonucleotide cassette into the EcoRI site of the mammalian plasmid expression vector pEE14 (Bebbington, C. R. & Hentschel, C. C. G., 1987, In: Glover, D. M., ed. DNA Cloning. Academic Press, San Diego. Vol 3, p163; Celltech Ltd., UK). Plasmid pEE14/IGF-1R/462 was transfected into Lec8 mutant CHO cells (Stanley, P. 1989, Molec. Cellul. Biol. 9:377-383) obtained from the American Tissue Culture Collection (CRL:1737), using Lipofectin (Gibco-BRL). Cell lines were maintained after transfection in glutamine-free medium (Glascow modification of Eagle's medium (GMEM; ICN Biomedicals, Australia) and 10% dialysed FCS (Sigma, Australia) containing 25 μM methionine sulphoximine (MSX; Sigma, Australia) as described (Bebbington, C. R. & Hentschel, C. C. G., 1987, In: Glover, D. M., ed. DNA Cloning. Academic Press, San Diego. Vol 3, p163). Transfectants were screened for protein expression by Western blotting and sandwich enzyme-linked immunosorbent assay (ELISA) (Cosgrove, L., et al., 1995,) using monoclonal antibody (Mab) 9E10 (Evan et al., 1985) as the capture antibody, and either biotinylated anti-IGF-1R Mab 24-60 or 24-31 for detection(Soos et al., 1992; gifts from Ken Siddle, University of Cambridge, UK). Large-scale cultivation of selected clones expressing IGF-1R/462 was carried out in a Celligen Plus bioreactor (New Brunswick Scientific, USA) containing 70 g Fibra-Cel Disks (Sterilin, UK) as carriers in a 1.25 L working volume. Continuous perfusion culture using GMEM medium supplemented with non-essential amino acids, nucleosides, 25 μM MSX and 10% FCS was maintained for 1 to 2 weeks followed by the more enriched DMEM/F12 without glutamine, with the same supplemention for the next 4-5 weeks. The fermentation production run was carried out three times under similar conditions, and resulted in an estimated overall yield of 50 mg of receptor protein from 430 L of harvested medium. Cell growth was poor during the initial stages of the fermentation when GMEM medium was employed, but improved dramatically following the switch to the more enriched medium. Target protein productivity was essentially constant during the period from ~100 to 700 h of the 760 h fermentation, as measured by ELISA using Mab 9E10 as the capture antibody and biotinylated Mab 24-31 as the developing antibody.

Soluble IGF-1R/462 protein was recovered from harvested fermentation medium by affinity chromatography on columns prepared by coupling Mab 9E10 to divinyl sulphone-activated agarose beads (Mini Leak;

Kem En Tec. Denmark) as recommended by the manufacturer. Mini-Leak Low and Medium affinity columns with antibody loadings of 1.5-4.5 mg/ml of hydrated matrix were obtained, with the loading range of 2.5-3 mg/ml giving optimal performance (data not shown). Mab 9E10 was produced by growing hybridoma cells (American Tissue Culture Collection) in serum-free medium in the Celligen Plus bioreactor and recovering the secreted antibody (4 g) using protein A glass beads (Prosep-A, Bioprocessing Limited, USA). Harvested culture medium containing IGF-1R/462 protein was adjusted to pH 8.0 with Tris-HCl (Sigma), made 0.02% (w/v) in sodium azide and passed at 3-5 ml/min over 50 ml Mab 9E10 antibody columns at 4° C. Bound protein was recovered by recycling a solution of 2-10 mg of the undecamer c-myc peptide EQKLISEEDLN (Hoogenboom et al., 1991) in 20 ml of Tris-buffered saline containing 0.02% sodium azide (TBSA). Between 65% and 75% of the product was recovered from the medium as estimated by ELISA, with a further 15-25% being recovered by a second pass over the columns. Peptide recirculation (~10 times) through the column eluted bound protein more efficiently than a single, slower elution. Residual bound protein was eluted with sodium citrate buffer at pH 3.0 into 1 M Tris HCl pH 8.0 to neutralize the eluant, and columns were re-equilibrated with TBSA.

Gel filtration over Superdex S200 (Pharmacia, Sweden), of affinity-purified material showed a dominant protein peak at ~63 kDa, together with a smaller quantity of aggregated protein (Figure 3a). The peak protein migrated primarily as two closely spaced bands on reduced , sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE; Figure 3b), reacted positively in the ELISA with both Mab 24-60 and Mab 24-31, and gave a single sequence corresponding to the N-terminal 14 residues of IGF-1R. No binding of IGF-1 or IGF-2 could be detected in the solid plate binding assay (Cosgrove et al., 1995, Protein Express Purif. 6:789-798). The IGF-1R/462 fragment was further purified by ion-exchange chromatography on Resource Q (Pharmacia, Sweden). Using shallow salt gradients, protein enriched in the slowest migrating SDS-PAGE band was obtained (data not shown), which formed relatively large, well-formed crystals (see below). Isoelectric focussing showed the presence of one major and two minor isoforms. Protein purified on Resource Q with an isocratic elution step of 0.14 M NaCl in 20 mM TrisCl at pH 8.0 (fraction 2, Figure 4) showed less heterogeneity on isoelectric focussing (Figure 4 inset) and SDS-PAGE (data not shown), and

produced crystals of sufficient quality for structure determination (see below).

Crystals were grown by the hanging drop vapour diffusion method using purified protein concentrated in Centricon 10 concentrators (Amicon Inc, USA) to 5-10 mg/ml in 10-20 mM Tris-HCl pH 8.0 and 0.02% (w/v) sodium azide, or 100 mM ammonium sulfate and 0.02% (w/v) sodium azide. Crystallization conditions were initially identified using the factorial screen (Jancarik, J. & Kim, S.-H.,1991, J Appl Cryst 24:409-411),and then optimised. Crystals were examined on an M18XHF rotating anode generator (Siemens, Germany) equipped with Franks mirrors (MSC, USA) and RAXIS IIC and IV image plate detectors (Rigaku, Japan).

From the initial crystallization screen of this protein, crystals of about 0.1 mm in size grew in one week. Upon refining conditions, crystals of up to 0.6 x 0.4 x 0.4 mm could be grown from a solution of 1.7-2.0 M ammonium sulfate, 0.1 M HEPES pH 7.5. The crystals varied considerably in shape and diffraction quality, growing predominantly as rhombic prisms with a length to width ratio of up to 5:1; but sometimes as rhombic bipyramids, the latter form being favoured when using material which had been eluted from the Mab 9E10 column at pH 3.0. Each crystal showed a minor imperfection in the form of very faint lines from the centre to the vertices. Protein from dissolved crystals did not appear to be different from the protein stock solution when run on an isoelectric focusing gel. Upon X-ray examination, the crystals diffracted to 3.0-4.0 Å and were found to belong to the space group $P2_12_12_1$ with a = 76.8 Å, b = 99.0 Å, c = 119.6 Å. In the diffraction pattern, the crystal variability noted above was manifest as a large (1-2°) and anisotropic mosaic spread, with concomitant variation in resolution. To improve the quality of the crystals, they were grown in the presence of various additives or were recrystallized. These methods failed to substantially improve the crystal quality although bigger crystals were obtained by recrystallization. The variability in crystal quality appeared to be due to protein heterogeneity, as demonstrated by the observation that more highly purified protein, eluted isocratically from the Resource Q column and showing one major band on isoelectric focusing (Figure 4 inset), produced crystals of sufficient quality for structure determination. These crystals diffracted to 2.6 Å resolution with cell dimensions, a = 77.0 Å, b = 99.5 Å, c = 120.1 Å and mosaic spread of 0.5°. Heavy metal derivatives of the IGF-

1R/462 crystals have been obtained and are leading to the determination of an atomic resolution structure of this fragment, which contains the L1, cysteine-rich and L2 domains of human IGF-1R.

EXAMPLE 2

Structure of the IGF-1R/1-462

Crystals were cryo-cooled to-170°C in a mother liquor containing 20% glycerol, 2.2 M ammonium sulfate and 100 mM Tris at pH 8.0. Native and derivative diffraction data were recorded on Rigaku RAXIS IIc or IV area detectors using copper Kα radiation from a Siemens rotating anode generator with Yale/MSC mirroroptics. The space group was $P2_12_12_1$ with a = 77.39 Å, b = 99.72 Å, and c = 120.29 Å. Data were reduced using DENZO and SCALEPACK (Otwinowski, Z. & Minor, W., 1996, Mode.Meth. Enzym. 276:307-326). Diffraction was notably anisotropic for all crystals examined.

Phasing by multiple isomorphous replacement(MIR) was performed with PROTEIN (Steigeman, W. Dissertation (Technical Univ. Munich, 1974) using anomalous scattering for both UO2 and PIP derivatives. Statistics for data collection and phasing are given in Table 1. In the initial MIR map regions of protein and solvent could clearly be seen, but the path of the polypeptide was by no means obvious. That map was subject to solvent flattening and histogram matching in DM (Cowtan, K.,1994, Joint CCP4 and ESF-EACBM newslett. Protein Crystallogr. 31:34-38). The structure was traced and rebuilt using O (Jones, T. A., et al., 1991, Acta Crystallogr. A47:110-119) and refined with X-PLOR 3.851 (Brunger, A. T., 1996, X-PLOR ReferenceManual 3.851, Yale Univ., New Haven, CT). After 5 rounds of rebuilding and energy minimisation the R-factor dropped to 0.279 and Rfree = 0.359 for data 7-2.6 Å resolution. The current model contains 458 amino acids and 3 N-linked carbohydrates but no solvent molecules. For residues with B(Ca) > 70, Å atomic positions are less reliable (37-42, 155-159, 305, 336-341, 404-406,453-458). There is weak electron density for residues 459-461, but the c-myc tail appears completely disordered.

The 1-462 fragment consists of the N-terminal three domains of IGF-1R (L1, cys-rich, L2), and contains regions of the molecule which dictate ligand specificity (17-23). The molecule adopts a reasonably extended structure (approximately 40 x 48 x 105 Å) with domain 2 (cys-rich region)

making contact along the length of domain 1 (L1) but very little contact with the third domain (L2) (see Figure 5). This leaves a space at the centre of the molecule of approximately 24 Å x 24 Å x 24 Å which is bounded on three sides by the three domains of the molecule. The space is of sufficient size to accommodate the ligand, IGF-1.

Table 1 Summary of Crystallographic data

Data set[a]	Resol. (Å)	Mean I/s	R_{merge}[b]	Completeness (multiplicity)	No. of sites	R_{cullis}[c]	Phasing power[d]	FOM[e]
Native	2.6	18.7	0.064	0.996 (4.1)				0.47 / 0.71
PIP	3.0	15.8	0.060	0.982 (2.2)	3	0.66	1.71	
UO2Ac2	4.5	7.5	0.095	0.989 (2.3)	2	0.82	1.17	

Refinement resolution (Å)	No of refl. (free)	No. of Atoms	R_{cryst}[f]	R_{free}[f]	Bonds[g] (Å)	Angles[g] (Å)
7.0-2.6	24270 (2693)	3903	0.237	0.304	0.017	0.048

[a] PIP, Di-μ-iodobis(ethylenediamine)diplatinum dinitrate; UO_2Ac_2, Uranyl acetate.

[b] $R_{merge} = \Sigma_h\Sigma_j |I_{h,j}-I_h| / \Sigma_h\Sigma_j I_h$, where $I_{h,j}$ is an intensity measurement j and I_h is the mean intensity for that reflection **h**.

[c] $R_{cullis} = \Sigma_h ||F_{PH}-F_P| - |F_{Hcalc}||/\Sigma_h||F_{PH}|-|F_P||$, where F_{PH}, F_P and F_{Hcalc} are, respectively, derivative, native and heavy atom structure factors for centric reflections **h**.

[d] Phasing power = $\Sigma_h |F_{Hcalc}|/\Sigma_h\varepsilon$, where F_{Hcalc} is defined above and ε is the lack of closure.

[e] FOM(figure of merit) = $\langle\cos(\Delta\alpha_h)\rangle$, where $\Delta\alpha_h$ is the error in the phase angle for reflection **h**. Values are given before and after density modification at 3.0 and 2.8 Å resolution, respectively.

[f] R_{cryst} and R_{free} are defined in Brunger, A.T. *XPLOR* reference manual 3.851 (Yale Univ., New Haven, CT, 1996)

8 r.m.s. deviation from ideal bond and angle-related (1-3) distances.

The L domains

Each of the L domains (residues 1-150 and300-460) adopts a compact shape (24 x 32 x 37 Å) consisting of a single-stranded right handed β-helix and capped on the ends by short α-helices and disulfide bonds. The body of the domain looks like a loaf of bread, with the base formed from a flat six-stranded β-sheet, 5 residues long and the sides being β-sheets three residues long (Figures 5 & 6). The top is irregular, but in places is similar for the two domains. The two domains are superposable with an rms deviation in Cα positions of 1.6 Å for 109 atoms (Figure 7). Although this fold is reminiscent of other β-helix proteins it is much simpler and smaller with very few elaborations, and thus it represents a new superfamily of domains. One notable difference between the two domains is that the indole ring of Trp 176 from the cys-rich region (Figure 6b) is inserted into the hydrophobic core of L1, and the C-terminal helix is only vestigial (Figure 8). For the insulin receptor family the sequence motif of residues which form the Trp pocket in L1 does not occur in L2 (Figure 6a). However in the EGF receptor, which has an additional cys-rich region after the L2 domain (14, 15), the pocket motif can be found in both L domains and the Trp is conserved in both cys-rich regions (Figure 6b).

The repetitive nature of the β-helix is reflected in the sequence and the first five turns were correctly identified by Bajaj, M., et al. (1987, Biochim.Biophys. Acta 916:220-226), the conserved Gly residues being found in turns making one bottom edge of the domain. However, their conclusions about the fold were incorrect. The"helix-like" repeat is actually a pair of bends at the top edge of the domain. In their Motif V, the Gly is not in a bend but is followed by the insertion of a conserved loop of 7-8 residues (see Figure 6a). Glycine is structurally important in the Gly bends as mutation of these residues compromises folding of the receptor [van der Vorm, E.R., et al., 1992, J. Biol. Chem. 267, 66-71; Wertheimer, E. et al., 1994, J. Biol. Chem. 269, 7587-7592].

Comparison of the L domains with other right-handed β-helix structures such as pectate lyase (Yoder, M. D., et al., 1993,.Structure, 1:241-251-1507) and the p22 tailspike protein (Steinbacher, S., et al., 1997, J.Mol. Biol. 267:865-880) shows some striking similarities as well as differences. In

all cases the ends of the domain are capped by α-helices, but the L domains also have a disulphide bond at each end to hold the termini. The other β-helix domains are considerably longer and have significant twist to their sheets, while the L domains have flat sheets. Although the sizes of the helix repeats are similar (here 24-25 residues vs 22-23 for pectate lyase) the cross-sections are quite different. The L domains have a rectangular cross-section, while pectate lyase and p22 tailspike protein are V-shaped, and have many, and sometimes quite large, insertions (Yoder, M. D., et al., 1993, Structure, 1:241-251-1507; Steinbacher, S., et al., 1997, J.Mol. Biol. 267:865-880). In the hydrophobic core a common feature is the stacking of aliphatic residues from successive turns of the β-helix, and near the C-terminus of each L domain there is also a short Asn ladder, reminiscent of the long Asn ladder observed in pectate lyase (Yoder, M. D., et al., 1993, Structure 1:241-251-1507). On the opposite side of the L domains the Gly bend, as well as the two bends and sheet preceding it, have no counterpart in the other β-helix domains. Thus although the L domains are built on similar principles to the other β-helix domains they constitute a separate superfamily.

The cys-rich domain

The cys-rich domain is composed of eight disulfide-bonded modules (Figure 6b), the first of which sits at the end of L1, while the remainder make a curved rod running diagonally across L1 and reaching to L2 (Figure 5). The strands in modules 2-7 run roughly perpendicular to the axis of the rod in a manner more akin to laminin (Stetefeld, J., et al.,1996, J.Mol.Biol. 257:644-657) than to TNF receptor (Banner, D. W., et al., 1993, Cell, 73:431-445), but the modular arrangement of the cys-rich domain is different to those of other cys-rich proteins for which structures are known. The first 3 modules of IGF-1R have a common core, containing a pair of disulfide bonds, but show considerable variation in the loops (Figure 6b). The connectivity of these modules is the same as in the first half of EGF (Cys 1-3and 2-4), but their structures do not appear to be closely related to any member of the EGF family. Modules 4 to 7 have a different motif, a β-finger, and best match residues 2152-2168 of fibrillin (Dowling, A. K., et al., 1996, Cell, 85:597-605). Each is composed of three polypeptide strands, the first and third being disulfide bonded and the latter two forming a β-ribbon. The β-ribbon of each β- finger module lines up antiparallel to form a tightly twisted 8-stranded β-sheet (Figures 5 and 8). Module 6 deviates from the common pattern,with

the first segment being replaced by an α-helix followed by a large loop that is likely to have a role in ligand binding (see below). As module 5 is most similar to module 7 it is possible that the four modules arose from serial gene duplications. The final module is a disulfide-linked bend of five residues.

The fact that the two major types of cys-rich modules occur separately implies that these are the minimal building blocks of cys-rich domains found in many proteins. Although it can be as short as 16 residues, the motif of modules 4-7 is clearly distinct, and capable of forming a regular extended structure. Thus cys-rich domains such as these can be considered as being made of repeat units each composed of a small number of modules.

Hormone binding

Attempts have been made to locate the IGF-1 (and insulin) binding site by examining natural (Taylor, S. I., 1992, Diabetes, 41:1473-1490) and site-directed mutants (Williams, P. F., et al., 1995, J. Biol. Chem. 270:3012-3016; Mynarcik, D. C et al., 1996, J. Biol. Chem. 271:2439-2442; Mynarcik, D. C., et al., 1997, J. Biol. Chem. 272:2077-2081), chimeric receptors (Andersen, A. S., et al., 1990, Biochemistry 29:7363-7366; Gustafson, T. A., & Rutter, W. J., 1990, J. Biol. Chem. 265:18663-18667; Schäffer, L., et al.,1993, J. Biol. Chem. 268:3044-3047; Schumacher, R., 1993, J. Biol. Chem. 268:1087-1094; Kjeldsen, T., et al., 1991, Proc. Natl Acad. Sci. USA, 88:4404-4408) and by crosslinking studies (Wedekind, F., et al., 1989, Biol. Chem Hoppe-Seyler, 370:251-258; Fabry, M., 1992, J. Biol. Chem. 267:8950-8956; Waugh, S. M., et al., 1989, Biochemistry, 28:3448-3458; Kurose, T., et al., 1994),.J. Biol. Chem.269:29190-29197-34). IGF-1R/IR chimeras not only show which regions of the receptors account for ligand specificity, but also provide an efficient means of identifying some parts of the hormone binding site. Paradoxically, regions controlling specificity are not the same for insulin and IGF-1. Replacing the first 68 residues of IGF-1R with those of IR confers insulin-binding ability on the chimeric IGF-1R (Kjeldsen, T., et al., 1991, Proc. Natl Acad. Sci. USA, 88:4404-4408), and replacing residues 198-300 in the cys-rich region of IR with the corresponding residues 191-290 of IGF-1R allows the chimeric receptor to bind IGF-1 (Schäffer, L., et al.,1993, J. Biol. Chem. 268:3044-3047). Thus a receptor can be constructed which binds both IGF-1 and insulin with near native affinity. From the structure it is clear that if the hormone bound in the central space it could contact both these regions.

From analysis of a series of chimeras examined by Gustafson, T. A., & Rutter, W. J. (J. Biol. Chem. 265:18663-18667, 1990), the specificity determinant in the cys-rich region can be limited further to residues 223-274. This region corresponds to modules 4-6, and includes a large and somewhat mobile loop (residues 255-263, mean B[Cα atoms] = 57 Å2) which extends into the central space (see Figure 5). In IR this loop is four residues bigger, and is stabilised by an additional disulfide bond (Schäffer, L. & Hansen, P.H.,1996, Exp. Clin. Endocrinol. Diabetes, 104: Suppl. 2, 89). The larger loop of IR may serve to exclude IGF-1 from the hormone binding site while allowing the smaller insulin molecule to bind. It is interesting to note that mosquito IR homologue, which has a loop two residues larger than the mammalian IRs, also appears to bind insulin but not IGF-1 (Graf, R., et al., 1997, Insect Molec.Biol. 6:151-163). Analysis of the structure indicates that the insulin/IGF-1 specificity is controlled by residues in this loop (amino acids 253-272 in IGF-1R; amino acids 260-283 in IR)

As chimeras only address residues which differ between the two receptors, a more precise analysis of the site can be obtained from single site mutants. In particular, from an alanine-replacement study, four regions of L1 important for insulin binding were identified (Williams, P. F., et al., 1995, J. Biol. Chem. 270:3012-3016). The first three are at similar positions on successive turns of the β-helix and the fourth lies on the conserved bulge on the large β-sheet. Thus there is a footprint for insulin binding to the L1 domain which lies on the first half of the large β-sheet facing into the central space. Residues further along the sheet which are conserved in IGF-1R could also be important. The conservative substitution of leucine for methionine at residue 119 of IR (113 of IGF-1R) causes a mild form of leprechaunism [Hone, J. et al., 1994, J. Med. Genet. 31, 715-716]. This residue is buried, and the mutation could perturb neighbouring residues to affect insulin binding.

The axis of the L2 domain is perpendicular to that of the L1 domain, and the N-terminal end of its β-helix is presented to the hormone-binding site. On this face of the L2 domain the only mutation studied so far is the naturally occurring IR mutant, S323L, which gives rise to Rabson-Mendehall syndrome and severe insulin resistance (Roach, P.,1994, Diabetes 43:1096-1102). As this mutant only affects insulin binding and not cell-surface expression, residue 323 of IR (residue 313 of IGF-1R) is probably at or near the binding site. Structurally this residue lies in the middle of a region

(residues 309-318 of IGF-1R) which is conserved in both IR and IGF-1R, and the surrounding region, 332-345 (of IGF-1R), is also quite well conserved in the these receptors (Figure 6a). Therefore this region is quite likely to form part of the hormone-binding site, but would not have been detected by chimeras. It is interesting to note that in this region IRR is not as well conserved as the other two receptors (Shier, P. & Watt, V.M., 1989, J.Biol.Chem. 264:4605-14608).

The distance from this putative hormone-binding region on L2 to that found on L1 is about 30 Å (Figure 5). Thus L1 and L2 appear too far apart to bind IGF-1 or insulin. However, in the crystal structure there is a deep cleft between part of the cys-rich domain (residue 262)and L2 (residue 305), and this cleft is occupied by a loop from a neighbouring molecule. Thus it seems probable that the position of the L2 domain in the receptor structure or the hormone-receptor complex adopts a different position with respect to the cys-rich domain than that found in the crystal. The movement required to bring L2 sufficiently close to L1 is small, namely a rotation of approximately 25° about residue 298.

A number of IR mutants have been identified which constitutively activate the receptor, and the majority of these are found in the α chain. Curiously all α chain mutants involve changes to or from proline or the deletion of an amino acid, implying that they cause local structural rearrangements. The mutation R86N is similar to wild type, but R86P reduces cell-surface expression and insulin binding while constitutively activating autophosphorylation [Grønskov, K. et al., 1993, Biochem. Biophys. Res. Commun. 192, 905-911]. The proline mutation probably disturbs residues preceding 87 which lie in the interface between the L1 and cys-rich domains, but it could also affect insulin binding. In the cys-rich domain residues 233, 281, 244 and 247 of IR are not conserved in IGF-1R (Figure 6b), yet L233P [Klinkhamer, M.P. et al., 1989, EMBO J. 8, 2503-2507], deletion of N281 [Debois-Mouthon, C. et al., 1996, J. Clin. Endochronol. Metab. 81, 719-727] or the triple mutant P243R, P244R and H247D [Rafaeloff, R. et al., 1989, J. Biol. Chem. 264, 15900-15904] cause constitutive kinase activation. Due to their locations each of these three mutants appears likely to compromise the folding of a β-finger domain and, in turn, the structural integrity of the rod-like cys-rich domain. The structural ramifications of these mutations could be significant for the whole receptor ectodomain, as disturbing the L1/cys-

rich interface or distorting the rod-like domain could affect the relative position of L1 and the cys-rich domain in this context.

L1 has been further implicated, as deletion of K121 on the opposite side of L1 from the cys-rich domain was also found to cause autophosphorylation [Jospe, N. et al., 1994, J. Clin. Endochronol. Metab. 79, 1294-1302]. By contrast this mutation does not affect insulin binding. Thus a possible mechanism emerges for insulin binding and signal transduction. When insulin binds between L1 and L2 it modifies the relative position of L1 and the cys-rich domain in the receptor, perhaps by hinge motion between L2 and the cys-rich domain like that suggested above, and the structural rearrangement is transmitted across the plasma membrane. In the absence of insulin the same signal can be initiated by mutations in the cys-rich region or at the L1/cys-rich interface, but at the expense on insulin binding. The signal can also be initiated more directly by mutations on the opposite side of L1 which affect the interaction of L1 with other parts of the ectodomain, possibly the other half of the receptor dimer.

Ligand Studies

Although there is no structural information about an IGF-1/IGF-1R complex a number of studies have probed the nature of this interaction. Results from cross-linking experiments with IGF-1 and insulin and their cognate receptors are consistent with the hormone binding site proposed above. For example B29 of insulin can be cross-linked to the cys-rich region (residues 205-316((Yip, C. C., et al., 1988, Biochim. Biophys. Res. Commun. 157:321-329) or the L1 domain (Wedekind, F., et al., 1989, Biol. Chem Hoppe-Seyler, 370:251-258). However, these two regions are reasonably well separated, and those studies may indicate that B29 is mobile. Other studies unfortunately do not map the site any more precisely.

Analogues and site-directed mutants of IGF-1 and IGF-2 have been more fruitful. IGF-1 and IGF-2 contain two extra regions relative to insulin, the C region between B and A and a D peptide at the C-terminus. For IGF-1, replacement of the C region by a four Gly linker reduced affinity for IGF-1R by a factor of 40 but increased affinity for IR 5-fold (Bayne, M.L.,et al., 1988, J. Biol.Chem. 264:11004-11008). Changes in affinity are consistent with the deletion in IGF-1 complementing differences in the cys-rich regions of IGF-1R and IR noted above. Mutation of residues either side of the C region (residue 24 for IGF-1 [Cascieri, M.A., et al., 1988, Biochemistry 27:3229-

3233], residues 27,43 for IGF-2, [Sakano, K., et al., 1991, J. Biol. Chem. 266:20626-20635]) also has deleterious effects on the affinity of the hormone for IGF-1R, as has truncation of the nearby D peptide in IGF-2 (Roth, B.V., et al., 1991, Biochem. Biophys. Res. Commun. 181:907-914).

Insulin has been extensively mutated. Binding studies [summarised in Kristensen, C. et al., 1997, J. Biol. Chem. 272, 12978-12983] indicate that insulin may bind its receptor via a hydrophobic patch (residues A2, A3, A19, B8, B11, B12, B15 and possibly B23 & B24). However this patch is normally buried, and requires the removal of the B chain's C-terminus from the observed position. Assuming IGF-1, IGF-2 and insulin bind their receptors in the same orientation, these data suggest an approximate orientation for the hormone when bound to the receptor.

One notable feature of IGF-1 and IGF-2 is the large number of charged residues and their uneven distribution over the surface. Basic residues are predominantly found in the C region and, in solution, this region is not well ordered in either IGF-1 or -2 (Sato, A., et al., 1993, Int J Peptide Protein Res. 41:433-440; Torres, A. M., et al., 1995, J. Mol. Biol. 248:385-401). In contrast the binding site of the receptor has a sizable patch of acidic residues in the corner where the cys-rich domain departs from L1. Other acidic residues which are specific to this receptor are found along the inside face of the cys-rich domain and the loop (residues 255-263) extending from module 6. Thus it is possible that electrostatic interactions play an important part in IGF-1 binding, with the C region binding to the acidic patch of the cys-rich region near L1 and the acidic patch on the other side of the hormone directed towards a small patch of basic residues (residues 307-310) on the N-terminal end of L2.

Although the structure of this fragment gives significant information about the nature of the hormone binding site, residues outside this region have also been shown to affect binding of ligand. A number of studies have implicated residues 704-715 of IR (Mynarcik, D. C et al., 1996, J. Biol. Chem. 271, 2439-2442; Kurose, T., et al., 1994, J. Biol. Chem.269:29190-29197). These residues could contact insulin on one of the sides left open in the current structure. Using insulin labelled at the B1 residue, Fabry, M., et al.,(1992, J. Biol. Chem. 267:8950-8956) cross-linked insulin to the fragment 390-488, part of which is not near the site as described. The explanation for this could be either the region 390-488 reaches back to the hormone binding

site, or this region could contact another hormone bound to the other half of the receptor. Further structural information is needed to establish how these other regions contact the hormone and to elucidate how binding of the hormone is communicated to the kinase inside the cell.

The structure of the L1-cys-rich-L2 domains of IGF-1R presented here represents the first structural information for the extracellular portion of a member of the insulin receptor family. The L domains display a novel fold which is common to the EGF receptor family, and the modular architecture of the cys-rich domain implies that smaller building blocks should be used to describe the composition of cysteine-rich domains. This fragment contains the major specificity determinants of receptors of this class for their ligands. It has an elongated structure with a space in the middle which could accommodate the ligand. The three sides of this site correspond to regions which have been implicated in hormone binding. Although other sites are present in the receptor ectodomain which interact with the ligand, this structure gives us an initial view of how the insulin, IGF-1 and IGF-2 might interact with their cell surface receptors to control their metabolic and mitogenic effects

Such information will provide valuable insight into the structure of the corresponding domains of the IR and insulin receptor-related receptor as well as members of the related EGFR family (Bajaj, M., et al., 1987, Biochim Biophys Acta 916:220-226; Ward, C. W. et al., 1995, Proteins: Struct Funct Genet 22:141-153).

EXAMPLE 3

Prediction of 3D Structure of the Corresponding Domains of IRR and IR Based on Structure of IGF-1R Fragment.

The sequence identities between the different members of the insulin receptor family are sufficient to allow accurate sequence alignments to facilitate 3D structure predictions by homology modelling. The alignments of the ectodomains of human IGF-1R, IR, and IRR are shown in Figure 9.

EXAMPLE 4

Single-Molecule Imaging of Human Insulin Receptor Ectodomain and its Fab Complexes

Cloning and expression of hIR -11 ectodomain protein

A full length clone of the human IR exon -11 form (hIR -11) was prepared by exchanging an Aat II fragment, nucleotides 1195 to 2987 , of the

exon +11 clone (plasmid pET; Ellis et al., 1986; gift from Dr W. J. Rutter, UCSF) of hIR (Ebina et al., 1985, *Cell* **40**, 747-758) with the equivalent Aat II fragment from a plasmid (pHIR/P12-1, ATCC 57493) encoding part of the extracellular domain and the entire cytoplasmic domain of hIR -11 (Ullrich et al., 1985, *Nature* **313** , 756-761). The ectodomain fragment of hIR -11 (2901 bp, coding for the 27 residue signal sequence and residues His1-Asn914) was produced by SalI and SspI digestion and inserted into the mammalian expression vector pEE6.HCMV-GS (Celltech Limited, Slough, Berkshire, UK) into which a stop codon linker had been inserted, as described previously (Cosgrove et al., 1995, *Protein Expression and Purification* **6**, 789-798) for the hIR exon +11 ectodomain.

The resulting recombinant plasmid pHIR II (2 μg) was transfected into glycosylation-deficient Chinese hamster ovary (Lec 8) cells (Stanley, 1989, *Molec. Cellul. Biol.* **9**, 377-383) with Lipofectin (Gibco-BRL). After transfection, the cells were maintained in glutamine-free medium GMEM (ICN Biomedicals, Australia) as described previously (Bebbington & Hentschel, 1987, In *DNA Cloning* (Glover, D., ectodomain.), Vol III, Academic Press, san Diego; Cosgrove et al., 1995, *Protein Expression and Purification* **6**, 789-798). Expressing cell lines were selected for growth in GMEM with 25 μM methionine sulphoximine (MSX, Sigma). Transfectants were screened for protein expression using sandwich ELISA with anti-IR monoclonal antibodies 83-7 and 83-14. Metabolic labelling of cells, immunoprecipitations, insulin binding assays and Scatchard analyses were performed as described previously for the exon +11 form of hIR ectodomain (Cosgrove et al., 1995, , *Protein Expression and Purification* **6**, 789-798).

hIR -11 ectodomain production and purification

The selected clone (inoculum of 1.28 x 108 cells) was grown in a spinner flask packed with 10 g of Fibra-cel disc carriers (Sterilin, U.K.) in 500 ml of GMEM medium containing 10% fetal calf serum (FCS) and 25 μM MSX. Selection pressure was maintained for the duration of the culture.

Ectodomain was recovered from harvested medium by affinity chromatography on immobilized insulin, and further purified by gel filtration chromatography on Superdex S200 (Pharmacia; 1 x 40 cm) in Tris-buffered saline containing 0.02% sodium azide (TBSA) as described previously (Cosgrove et al., 1995, *Protein Expression and Purification* **6**, 789-798). Solutions of purified hIR -11 ectodomain were stored at 4° C prior to use.

Production of Fab fragments and their complexes with ectodomain

Purification of Mabs 83-7, 83-14 and 18-44 from ascites fluid by affinity chromatography using Protein A-Sepharose, and the production of Fabs, were based on the methodologies described in Coligan et al.,1993, Current Protocols in Immunology, Vol 1, pp 2.7.1-2.8.9, Greene Publishing Associates & Wiley - Interscience, John Wiley and Sons. Fab was produced from monoclonal antibody by mercuripapain digestion for 1-4 h, followed by gel filtration on Superdex S200. Products were monitored by reducing and non-reducing SDS-PAGE. For 83-7 Mab, an IgG Type 1 monoclonal antibody, the bivalent (Fab)2' isolated by this method was reduced to monovalent Fab 83-7 by mild reduction with mM L-cysteine.HCl in 100 mM Tris pH 8.0 (Coligan et al., 1993, Current Protocols in Immunology, Vol 1, pp 2.7.1-2.8.9, Greene Publishing Associates & Wiley - Interscience, John Wiley and Sons).

Complexes of Fab with hIR -11 ectodomain were produced by mixing ~ 2.5 to 3.5 molar excess of Fab with hIR -11 ectodomain at ambient temperature in TBSA at pH 8.0. After 1-3 h, the complex was separated from unbound Fab by gel filtration over a Superdex S200 column in the same buffer.

Electron microscopy

Uncomplexed hIR -11 ectodomain and the Fab complexes described above were diluted in phosphate-buffered saline (PBS) to concentrations of the order of 0.01-0.03 mg/ml. Prior to dilution, 10% glutaraldehyde (Fluka) was added to the PBS to achieve a final concentration of 1% glutaraldehyde. Droplets of ~ 3ml of this solution were applied to thin carbon film on 700-mesh gold grids after glow-discharging in nitrogen for 30 s. After 1 min. the excess protein solution was drawn off and followed by application and withdrawal of 4-5 droplets of negative stain [2% uranyl acetate (Agar), 2% uranyl formate (K and K), 2% potassium phosphotungstate (Probing and Structure) adjusted to pH 6.0 with KOH, or 2% methylamine tungstate (Agar) adjusted to pH 6.8 with NH4OH]. In the case of both uranyl acetate and uranyl formate staining, an intermediate wash with 2 or 3 droplets of PBS was included prior to application of the stain. The grids were air-dried and

then examined at 60kV accelerating voltage in a JEOL 100B transmission electron microscope at a magnification of 100,000x. It was found that there was a typical thickness of negative stain in which Fabs were most easily seen. Hence areas for photography had to be chosen from particular zones of the grid. Electron micrographs were recorded on Kodak SO-163 film and developed in undiluted Kodak D19 developer. The electron-optical magnification was calibrated under identical imaging conditions by recording single-molecule images of the antigen-antibody complex of influenza virus neuraminidase heads and NC10 MFab (Tulloch et al., 1986, *J.Mol. Biol.* **190**, 215-225; Malby et al., 1994, *Structure*, **2**, 733-746).

Image processing

Electron micrographs showing particles in a limited number of identifiable projections were chosen for digitisation. Micrographs were digitised on a Perkin-Elmer model 1010 GMS PDS flatbed scanning microdensitometer with a scanning aperture (square) size of 20 mm and stepping increment of 20 mm corresponding to a distance of 0.2 nm on the specimen. Particles were selected from the digitised micrograph using the interactive windowing facility of the SPIDER image processing system (Frank et al., 1996, *J. Struct. Biol.* **116**, 190-199). Particles were scaled to an optical density range of 0.0 - 2.0 and aligned by the PSPC reference-free alignment algorithm (Marco et al., 1996, *Ultramicroscopy*, **66**, 5-10). Averages were then calculated over a subset of correctly aligned particles chosen interactively as being representative of a single view of the particle. The final average image presented here is derived from a library of 94 images.

Biochemical characterization of expressed hIR -11 ectodomain

The recombinant protein examined corresponded to the the first 914 residues of the 917 residue ectodomain of the exon -11 form of the human insulin receptor (Ullrich et al., 1986, *Nature* **313** , 756-761). Expressed protein was shown, by SDS-PAGE and autoradiography of immunoprecipitated product from metabolically labelled cells, to exist as a homodimeric complex of ~270 - 320 kDa apparent mass, which dissociated under reducing conditions into monomeric α and β' subunits of respective apparent mass ~120 kDa and ~35 kDa (data not shown).

Purified hIR -11 ectodomain, expressed in Lec8 cells and purified by affinity chromatography on an insulin affinity column, eluted as a symmetrical peak on a Superdex S200 gel filtration column (Figure 10). The

protein eluted with an apparent mass of ~400 kDa, calculated from a standard curve generated by the elution positions of standard proteins (not shown). As expected for protein expressed in Lec 8 cells, whose glycosylation defect produces truncated oligosaccharides (Stanley, 1989, . *Molec. Cellul. Biol.* **9**, 377-383), this value is less than the apparent mass (450 - 500 kDa) reported for hIR +11 ectodomain expressed in wild-type CHO-K1 cells (Johnson et al., 1988, *Proc. Natl Acad. Sci USA* **85**, 7516-7520; Cosgrove et al., 1995, *Protein Expression and Purification* **6**, 789-798).

Radioassay of insulin binding to purified ectodomain gave linear Scatchard plots and Kd values of 1.5 - 1.8 x 10-9 M, similar to the values of 2.4 - 5.0 x 10-9 M reported for the hIR -11 ectodomain (Andersen et al., 1990, *Biochemistry* **29**, 7363-7366; Markussen et al., 1991, *J. Biol. Chem.* **266**, 18814-18818; Schaffer, 1994, *Eur. J. Biochem.* **221**, 1127-1132) and the values of ~1.0 - 5.0 x 10-9 M reported for the hIR +11 ectodomain (Schaefer et al., 1992, *J. Biol. Chem.* **267**, 23393-23402; Whittaker et al., 1994, *Molec. Endocrinol.* **8**, 1521-1527; Cosgrove et al., 1995, *Protein Expression and Purification* **6**, 789-798).

Expression of hIGF-1R ectodomain

Cloning, expression and purification of this protein used elements common to those described for hIR -11 ectodomain (Cosgrove et al., 1995, *Protein Expression and Purification* **6**, 789-798), and resulted in purified product that was recognised by receptor-specific Mabs 17-69, 24-31 and 24-60 (Soos et al., 1992, *J. Biol. Chem.* **267**, 12955-63) and was composed of α and β' subunits of mass similar to those of hIR ectodomain.

Preparation of hIR -11 ectodomain/MFab complexes

A complex of hIR -11 ectodomain and Fab from antibody 83-14 eluted as a symmetrical peak of 460 -500 kDa (Figure 10), as did complexes generated from a mixture of hIR -11 ectodomain with Fab from antibody 18-44 and a mixture of hIR -11 ectodomain with Fab 83-7 (not shown). A co-complex of ectodomain with Fabs from antibodies 18-44 and 83-14 eluted at ~ 620 kDa, as did a co-complex with MFabs 83-14/83-7 and another with MFabs 83-7/18-44 (not shown). A complex of hIR -11 ectodomain with all three MFab derivatives, 18-44, 83-7 and 83-14, eluted at an apparent mass of ~ 710 kDa (Figure 10).

Electron microscopy

Imaging of hIR -11 and hIGF-1R ectodomains

Single-molecule imaging of uncomplexed dimeric hIR -11 ectodomain was carried out under a variety of negative staining conditions, which emphasised different aspects of the structure of the molecular envelope. Images obtained by this investigation are depicted in Figure 11.

The least aggressive or penetrative stain was potassium phosphotungstate (KPT) , which revealed consistent globular particles with very little internal structure other than a suggestion of a division into two parallel bars. Staining with methylamine tungstate also revealed the parallel bar images.

Further investigation using progressively more penetrative, but also potentially more disruptive, stains confirmed the observations above. Staining with uranyl acetate and uranyl formate showed the separation of the parallel bars most clearly, but uranyl acetate showed evidence of disrupting the structure of the particles, i.e. a decrease in the consistency of the particle shape and a tendency for particles to look unravelled or denatured despite having been subjected to chemical cross-linking prior to staining. In areas of thicker stain, parallel bars predominated, whereas in more thinly stained regions, U-shaped particles could be identified, sometimes outnumbering the parallel-bar structures (see Figure 11).

Imaging of hIR -11 ectodomain complexed with 83-7 MFab

This complex was particularly noteworthy for the consistency of the form of the particles, especially under the gentler staining conditions afforded by stains such as KPT and methylamine tungstate. The particles were interpreted as having been restricted in the views they presented, after air-drying on the carbon support film, by the almost diametrically opposite binding of the two Fab arms to the antigen to form a highly elongated complex structure. Under these conditions three distinct views could be recognised (see Figure 11). Two views (interpreted as top/down/bottom-up) show the Fab arms displaced clockwise or anti-clockwise as extensions of the parallel plates with two-fold symmetry. The third view shows an image with the two Fab arms in line roughly through the centre of the receptor on its opposite sides, interpreted as a side projection of binding half-way up the plates.

The use of aggressive uranyl stains operating at lower pHs revealed internal structure of the molecular envelope at the expense of consistency of the particle morphology. For example, staining with uranyl acetate or uranyl

formate showed that parallel bars can be seen in particles in which the Fab arms are displaced either clockwise or anticlockwise but not where the intermediate central or axial position of the two Fab arms is presented in projection. These observations show 83-7 MFab binding roughly half-way up the side-edge of each hIR -11 ectodomain plate. The epitope recognised by Mab 83-7 has been mapped to the cys-rich region, residues 191-297, by analysis of chimeric receptors (Zhang and Roth, 1991, *Proc. Natl. Acad. Sci. USA* **88**, 9858-9862).

Imaging of hIR -11 ectodomain complexed with either 83-14 MFab or 18-44 MFab

Complexes were formed with Fabs from the most insulin-mimetic antibody Mab 83-14. Projections showing the Fab arms bound to and extending out from near the base of the U-shaped particles were identified. A second field of particles showed objects composed of two parallel bars as observed for the undecorated ectodomain, with Fab arms projecting obliquely from diametrically opposite extremities (see Figure 11). Similar but less definitive images were also seen when MFab 18-44 was bound to hIR -11 ectodomain. The epitope for Mab 83-14 is between residues 469-592 (Prigent et al., 1990) in the connecting domain. This domain contains one of the disulphide bonds (Cys524-Cys524) between the two monomers in the IR dimer (Schaffer and Ljungqvist, 1992, *Biochem. Biophys. Res. Commun.* **189**, 650-653). The epitope for Mab 18-44 is a linear epitope, residues 765-770 (Prigent et al., 1990, . *J. Biol. Chem.* **265**, 9970-9977) in the β-chain, near the end of the insert domain (O'Bryan et al., 1991, *Mol. Cell. Biol.* **11**, 5016-5031). The insert domain contains the second disulphide bond connecting the two monomers in the IR dimer (Sparrow et al., 1997, *J. Biol. Chem.*, 272, 29460-29467).

Imaging of hIR -11 ectodomain co-complexed with two different MFabs per monomer

The double complex of hIR -11 ectodomain with MFabs 83-7 and 18-44 was stained with 2% KPT at pH 6.0, and revealed the molecular envelopes. The particle appears complex in shape, and can assume a number of different orientations on the carbon support film, giving rise to a number of different projections in the micrograph. The predominant view is of an asymmetric X-shape (some examples circled). It shows the 83-7 MFab arms bound at opposite ends of the parallel bars with the two 18-44 MFabs

appearing as shorter projections extending out from either side of each ectodomain.

Images of the double complex of hIR -11 ectodomain with 83-7 and 83-14 MFabs gave X-shaped images similar to those seen with the 83-7/18-44 double complex. In contrast the double complex of hIR -11 ectodomain with 18-44 and 83-14 MFabs did not present the characteristic asymmetric X-shapes described above. Instead, the molecular envelope appeared to be elongated in many views, with only an occasional X-shaped projection. While a detailed interpretation of these images would be premature, it is clear that MFabs 18-44 and 83-14, two of the more potent insulin mimetic antibodies (Prigent et al., 1990, *J. Biol. Chem.* **265**, 9970-9977), can bind simultaneously to the receptor.

Imaging of hIR -11 ectodomain co-complexed with three different MFabs per monomer

A field of particles from a micrograph of hIR -11 ectodomain were complexed simultaneously with MFabs 83-7, 83-14 and 18-44. In the thicker stain regions the molecular envelope was X-shaped, and looked very similar to that of the double complexes of hIR -11 ectodomain with either 83-7 and 18-44 or 83-7 and 83-14. However, in the more thinly stained regions particles of greater complexity were visible, and it was possible occasionally to identify that there are in fact more than four MFabs bound to the ectodomain dimer.

The single-molecule imaging of hIR -11 ectodomain presented here suggests a molecular envelope for this dimeric species significantly different from that of any previously published study. However, an unequivocal determination of the molecular envelope even from the present study is not entirely straightforward. A major complicating factor here has been the relative fragility of the expressed ectodomain when exposed to the rigors of electron microscope preparation by negative staining. For example, staining with potassium phosphotungstate (KPT, pH 6.0-7.0) frequently suggested a denaturation of the dimeric molecules, but when appropriate conditions were satisfied, good seemingly interpretable molecular envelope images were achieved; staining with methylamine tungstate (pH ~7.0) supported the best KPT molecular envelope images, but had the suggestion of a swelling of the molecular structure at neutral pH; and the acid-pH stains of uranyl acetate (pH ~4.2) and uranyl formate (pH~3.0), with their ability to penetrate the

ectodomain structure, appeared to illuminate not so much the molecular envelope as the zones of high projected protein density within the dimer.

An amalgam of impressions from these various staining regimens has led to the following interpretation of single-molecule images of these undecorated, or naked, dimers: the predominant dimeric molecular image encountered here has been that of "parallel bars"of projected protein density. This view is so predominant, indeed, that it suggests there is either a single preferred orientation of the molecules on the glow-discharged carbon support film, or that this impression of parallel bars of density may represent a mixture of superficially similar structure projections, with the subtleties of these different projections being masked by the relatively coarse resolution of this single-molecule direct imaging. The impression of parallel bars of projected protein density is particularly predominant in regions of thicker negative stain. A second view of the molecular envelope, appreciably less well represented in regions of thicker stain but predominant in regions of thin staining, is that of 'open' U's, or V's. These two views of hIR -11 ectodomain were supported by the single-molecule imaging of hIGF-1R ectodomain under comparable conditions of negative staining.

If the assumption is made that these two recognisable projected views, that of parallel bars and of open U's/V's, are different views of the same dimeric molecule, an assumption strongly supported by the MFab complex imaging, a coarse model of the molecular envelope can be rationalized. The model structure is roughly that of a cube, composed of two almost-parallel plates of high protein density, separated by a deep cleft of low protein main-chain and side-chain density able to be penetrated by stain, and connected by intermediate stain-excluding density near what is assumed here to be their base (that is, nearest the membrane-anchoring region). The width of the low-density cleft appears to be of the order of 30-35Å, sufficient to accommodate the binding of the insulin molecule of diameter ca. 30Å, although we have no electron microscopical evidence to support insulin-binding in this cleft at this stage.

It has been established through imaging of bound 83-7 MFab that there is a dimeric two-fold axis normal to the membrane surface between these plates of density. Occasionally, dimer images display a relative displacement of the bars of density, interpreted here as a limited capacity for a shearing of the interconnecting zone between the two plates along their

horizontal axis parallel to the membrane; other images show bars skewed from parallel, implying a limited capacity for the plates to rotate independently around the two-fold axis, again via this interconnecting zone. These two observations each suggest a relatively flexible connectivity between the dimer plates in the membrane-proximal region of intermediate protein density, which could possibly contribute to the transmembrane signalling process.

The approximate overall measured dimensions of the ectodomain dimer are 110 x 90 x 120Å, calibrated against the dimensions of imaged influenza neuraminidase heads, known from the solved X-ray structure (Varghese et al., 1983, *Nature* **303**, 35-40). It can be noted that there is a compatibility here between the molecular weights and molecular dimensions of these two molecular species: the compact tetrameric influenza neuraminidase heads of Mr ~200 kDa occupy a volume almost 100 x 100 x 60 Å; the more open dimeric insulin receptor ectodomains of similar Mr ~240 kDa imaged here occupy a volume approximately 110 x 90 x 120 Å , roughly twice that of the neuraminidase heads, accommodating the slightly higher molecular weight and substantial central low-density cleft.

The low-resolution roughly cubic compact structure proposed here differs substantially from the T-shaped model proposed by Christiansen et al. (1991, *Proc. Natl. Acad. Sci. U. S. A.* **88**, 249-252) and Tranum-Jensen et al., (1994, *J. Membrane Biol.* **140**, 215-223) for the whole receptor and the elongated model proposed by Schaefer et al. (1992, *J. Biol. Chem.* **267**, 23393-23402) for soluble ectodomain. Significantly, those previous studies did not provide any convincing independent electron microscopical evidence that their imaged objects were in fact insulin receptor.

In the present study, the identity of the imaged molecules as hIR -11 ectodomain has been confirmed by imaging complexes of the dimer with Fabs of the three well-established conformational Mabs against native hIR, 83-7, 83-14 and 18-44 (Soos et al.,1986, *Biochem. J.* **235**, 199-208; 1989, *Proc. Natl Acad. Sci. USA* **86**, 5217-5221), bound singly and in combination. In all these instances, virtually every particle in the field of view exhibited MFab decoration through binding to conformational epitopes, establishing not only the identity of the imaged particles but also the conformational integrity of the expressed ectodomains. Furthermore, the cleanliness and uniformity of these hIR -11 ectodomain preparations, both naked and decorated, visualised

here by electron microscopy demonstrate their high suitability for X-ray crystallization trials.

The known flexibility of the Fab arms exacerbates image-to-image variability beyond the limited extent already described for the undecorated dimeric ectodomains, complicating any precise interpretation of these antigen-antibody complexes. Such molecular flexibility also renders largely impractical any single-molecule computer image averaging to facilitate image interpretation, progressively more so with the higher order antigen-antibody complexes studied here.

The most readily interpretable of these images, showing least image-to-image variability, are those of 83-7 MFab bound to dimers where, fortuitously, the antigen-antibody complex is constrained in its degrees of rotational freedom on the carbon support film. Many projected images show the two Fab arms in line roughly through the centre of the antigen on its opposite sides, interpreted as a side projection of binding half-way up the plates from their membrane-proximal base. Other sub-sets of images show the two Fab arms still parallel but displaced clockwise or anticlockwise with 2-fold symmetry, each Fab approximating an extension of one of the parallel bars of antigen density, interpreted here as representing top or bottom projections along the 2-fold axis. The third projection, along the axis of the Fab arms, could not be sampled here because of the constraining geometry of this molecular complex. These observations suggest binding of 83-7 MFab roughly half-way up the side-edge of the hIR -11 ectodomain plate. This then allows an initial attempt at spatially mapping the 83-7 MFab epitope, which has been sequence-mapped to residues 191-297 in the cys-rich region of the insulin receptor (Zhang and Roth, 1991, *Proc. Natl. Acad. Sci. USA* **88**, 9858-9862). The spatial separation and relative orientations of the two binding epitopes of Mab 83-7 on the hIR -11 ectodomain dimer as indicated here appear inconsistent with the proposal that Mab 83-7 could bind intramolecularly to hIR (O'Brien et al., 1987, *Biochem J.* **6**, 4003-4010).

Decoration of the ectodomain dimer with 83-7 MFab established that the two plates of high protein-density are arranged with 2-fold symmetry. Decoration with either 83-14 or 18-44 MFab , on the other hand, allowed sampling of the third projection of the ectodomain dimer precluded by 83-7 MFab binding. Significantly, this third view established unequivocally the U-shaped projection of the hIR -11 ectodomain dimer, something which was

only able to be assumed with the undecorated ectodomain images. Further, this projection has allowed a rough spatial mapping close to the base of the U-shaped dimer for the epitopes recognised by 83-14 MFab (residues 469-592, connecting domain) and 18-44 MFab (residues 765-770, b-chain insert domain; exon 11 plus numbering, Prigent et al., 1990, *J. Biol. Chem.* **265**, 9970-9977).

Inherent in the model structure is the implication that, with the two-fold axis aligned normal to the membrane surface, the mouth of the low-density cleft where insulin binding may occur would lie most distant from the transmembrane anchor, whilst the zone of intermediate density connecting the two high-density plates would be in close proximity to the membrane. It follows, in this model, that the L1/cys-rich/L2 domains(Bajaj et al., 1997, *Biochim. Biophys. Acta* **916**, 220-226; Ward et al.,1995, *Proteins: Struct., Funct., Genet.* **22**, 141-153), which comprise much of the insulin-binding region (see Mynarcik et al., 1997, . *J. Biol. Chem.* **272**, 2077-2081), most probably lie in the membrane-distal upper halves of the two plates, whilst the membrane-proximal lower halves contain the connecting domains, the fibronectin-type domains, the insert domains and the interchain disulphide bonds (Schaffer and Ljungqvist, 1992, *Biochem. Biophys. Res. Commun.* **189**, 650-653; Sparrow et al., 1997, *J. Biol. Chem.*, 272, 29460-29467). Such a disposition of domains is supported by the images seen with the single MFab decoration, the 83-7 MFab epitope in the cys-rich region being spatially mapped roughly half-way up the side-edge of the ectodomain plates, and the 83-14 and 18-44 MFab epitopes (connecting domain and β-chain insert domain, respectively) being mapped near the base of the plates. Our preference is for a single a-b¢ monomer to occupy a single plate, although the possibility of a single monomer straddling the two plates of protein density cannot be discounted.

The more complex images involving co-binding of two, and even more so of all three, MFabs to each monomer of the ectodomain dimer are not easily interpretable with respect to relative domain arrangements within the monomer at present, not least of all because of the difficulty of finding conditions of negative staining that will simultaneously maintain the integrity of the Fab binding while highlighting recognisable and reproducible details of the internal structure of the dimeric IR ectodomain.

The data presented here demonstrate the ability of single-molecule imaging to give an initial insight into the topology of multidomain structures such as the ectodomain of hIR, and the value of combining this technique with that of either single or multiple monoclonal Fab attachment per monomer as a potential means of epitope, and domain, mapping of the structure. By imaging Fab complexes of other members of the family, such as hIGF-1R ectodomain, and combining available sequence-mapped epitope information with that presented here, a more comprehensive understanding of domain arrangements within the IR family ectodomains should be forthcoming.

EXAMPLE 5

Structure-Based Design of Ligands for the IGF Receptor as Potential Inhibitors of IGF Binding

The structure of IGF receptor can be considered as a filter or screen to design, or evaluate, potential ligands for the receptor. Those skilled in the art can use a number of well known methods for de novo ligand design, such as GRID, GREEN, HSITE, MCSS, HINT, BUCKETS, CLIX, LUDI, CAVEAT, SPLICE, HOOK, NEWLEAD, PRO_LIGAND, ELANA, LEGEND, GenStar, GrowMol, GROW, GEMINI, GroupBuild, SPROUT, and LEAPFROG, to generate potential agonists or antagonists for IGF-1R. In addition, the IGF-1R structure may be used as a query for database searches for potential ligands. The databases searched may be existing eg ACD, Cambridge Crystallographic, NCI, or virtual. Virtual databases, which contain very large numbers (currently up to 10^{12}) of chemically reasonable structures, may be generated by those skilled in the art using techniques such as DBMaker, ChemSpace, TRIAD and ILIAD.

The IGFR structure contains a number of sites into which putative ligands may bind. Search strategies known to those skilled in the art may be used to identify putative ligands for these sites. Examples of two suitable search strategies are described below:

(i) *Database Search*

The properties of key parts of the putative site may be used as a database search query. For example, the Unity 2.x database software may be used. A flexible 3D search can be run in which a "directed tweak" algorithm is used to find low energy conformations of potential ligands which satisfy the query.

(ii) *De novo design of ligands*

The Leapfrog algorithm as incorporated in the software package, Sybyl version 6.4.2 (Tripos Associates, St Louis), may be used to design potential ligands for IGF-1R sites. The coordinates of residues around the site may be taken from the x-ray structure, hydrogens and charges (Kollman all atom dictionary charges) added. From the size, shape and properties of the site, a number of potential ligands may be proposed. Leapfrog may be used to optimize the conformation of ligands and position on the site, to rank the likely strength of binding interactions with IGF-1R, and to suggest modifications to the structures which would have enhanced binding.

It is also possible to design ligands capable of interacting with more than one site. One way in which this may be done is by attaching flexible linkers to ligands designed for specific sites so as to join them. The linkers may be attached in such a way that they do not disrupt the binding to individual sites.

All references cited above are incorporated herein in their entirety by reference.

It will be appreciated by persons skilled in the art that numerous variations and/or modifications may be made to the invention as shown in the specific embodiments without departing from the spirit or scope of the invention as broadly described. The present embodiments are, therefore, to be considered in all respects as illustrative and not restrictive.

Claims:

1. A method of designing a compound able to bind to a molecule of the insulin receptor family and to modulate an activity mediated by the molecule, including the step of assessing the stereochemical complementarity between the compound and the receptor site of the molecule, wherein the receptor site includes:

(a) amino acids 1 to 462 of the receptor for IGF-1, having the atomic coordinates substantially as shown in Figure 1;

(b) a subset of said amino acids, or;

(c) amino acids present in the amino acid sequence of a member of the insulin receptor family, which form an equivalent three-dimensional structure to that of the receptor molecule as depicted in Figure 1.

2. A method according to claim 1, in which the compound is selected or modified from a known compound identified from a database.

3. A method according to claim 1, in which the compound is designed so as to complement the structure of the receptor molecule as depicted in Figure 1.

4. A method according to any one of claims 1 to 3, in which the compound has structural regions able to make close contact with amino acid residues at the surface of the receptor site lining the groove, as depicted in Figure 2.

5. A method according to any one of claims 1 to 4, in which the compound has a stereochemistry such that it can interact with both the L1 and L2 domains of the receptor site.

6. A method according to any one of claims 1 to 4, in which the compound has a stereochemistry such that it can interact with the L1 domain of a first monomer of the receptor homodimer, and with the L2 domain of the other monomer of the receptor homodimer.

7. A method according to any one of claims 1 to 4, in which the interaction of the compound with the receptor site alters the position of at least one of the

L1, L2 or cysteine-rich domains of the receptor molecule relative to the position of at least one of the other of said domains.

8. A method according to claim 7, in which the compound interacts with the β sheet of the L1 domain of the receptor molecule, thereby causing an alteration in the position of the L1 domain relative to the position of the cysteine-rich domain or of the L2 domain.

9. A method according to claim 7, in which the compound interacts with the receptor site in the region of the interface between the L1 domain an the cysteine-rich domain of the receptor molecule, thereby causing the L1 domain and the cysteine-rich domain to move away from each other.

10. A method according to claim 7, in which the compound interacts with the hinge region between the L2 domain and the cysteine-rich domain of the receptor molecule, thereby causing an alteration in the positions of the L2 domain and the cysteine-rich domain relative to each other.

11. A method according to any one of claims 1 to 10, in which the stereochemical complementarity between the compound and the receptor site is such that the compound has a K_b for the receptor side of less than 10^{-6}M.

12. A method according to claim 11, in which the K_b is less than 10^{-8}M.

13. A method according to any one of claims 1 to 12, in which the compound has the ability to increase an activity mediated by the receptor molecule.

14. A method according to any one of claims 1 to 12, in which the compound has the ability to decrease an activity mediated by the receptor molecule.

15. A method according to claim 14, in which the stereochemical interaction between the compound and the receptor site is adapted to prevent the binding of a natural ligand of the receptor molecule to the receptor site.

16. A method according to claim 14 or claim 15, in which the compound has a K_1 of less than 10^{-6}M.

17. A method according to claim 16, in which the compound has a K_1 of less than 10^{-8}M.

18. A method according to claim 17, in which the compound has a K_1 of less than 10^{-9}M.

19. A method according to any one of claims 1 to 18, in which the receptor is the IGF-1R.

20. A method according to any one of claims 1 to 18, in which the receptor is the insulin receptor.

21. A computer-assisted method for identifying potential compounds able to bind to a molecule of the insulin receptor family and to modulate an activity mediated by the molecule, using a programmed computer including a processor, an input device, and an output device, including the steps of:

(a) inputting into the programmed computer, through the input device, data comprising the atomic coordinates of the IGF-1R molecule as shown in Figure 1, or a subset thereof;

(b) generating, using computer methods, a set of atomic coordinates of a structure that possesses stereochemical complementarity to the atomic coordinates of the IGF-1R site as shown in Figure 1, or a subset thereof, thereby generating a criteria data set;

(c) comparing, using the processor, the criteria data set to a computer database of chemical structures;

(d) selecting from the database, using computer methods, chemical structures which are structurally similar to a portion of said criteria data set; and

(e) outputting, to the output device, the selected chemical structures which are similar to a portion of the criteria data set.

22. A computer-assisted method according to claim 21, in which the method is used to identify potential compounds which have the ability to decrease an activity mediated by the receptor.

23. A computer-assisted method according to claim 21 or claim 22, which further includes the step of selecting one or more chemical structures from step (e) which interact with the receptor site of the molecule in a manner which prevents the binding of natural ligands to the receptor site.

24. A computer-assisted method according to any one of claims 21 to 23, which further includes the step of obtaining a compound with a chemical structure selected in steps (d) and (e), and testing the compound for the ability to decrease an activity mediated by the receptor.

25. A computer-assisted method according to claim 21, in which the method is used to identify potential compounds which have the ability to increase an activity mediated by the receptor molecule.

26. A computer-assisted method according to claim 25, further including the step of obtaining a molecule with a chemical structure selected in steps (d) and (e), and testing the compound for the ability to increase an activity mediated by the receptor.

27. A computer-assisted method according to any one of claims 21 to 26, in which the receptor is the IGF-1R.

28. A computer-assisted method according to any one of claims 21 to 26, in which the receptor is the insulin receptor.

29. A method of screening of a putative compound having the ability to modulate the activity of a receptor of the insulin receptor family, including the steps of identifying a putative compound by a method according to any one of claims 1 to 29, and testing the compound for the ability to increase or decrease an activity mediated by the receptor.

30. A method according to claim 29, in which the test is carried out *in vitro*.

31. A method according to claim 29, in which the test is a high throughput assay.

32. A method according to claim 29, in which the test is carried out *in vivo*.

33. A method according to claim 30, in which the test is carried out *in vivo*.

Figure 1

ATOM	1	CB	GLU	1	55.907	11.986	66.300	1.00	59.11	AAAA C
ATOM	2	CG	GLU	1	56.138	11.019	65.162	1.00	78.17	AAAA C
ATOM	3	CD	GLU	1	57.382	11.319	64.321	1.00	85.10	AAAA C
ATOM	4	OE1	GLU	1	58.404	10.754	64.796	1.00	86.18	AAAA O
ATOM	5	OE2	GLU	1	57.424	12.013	63.270	1.00	78.70	AAAA O
ATOM	6	C	GLU	1	53.508	12.557	66.350	1.00	48.46	AAAA C
ATOM	7	O	GLU	1	52.685	11.863	65.784	1.00	51.27	AAAA O
ATOM	10	N	GLU	1	54.256	10.338	67.159	1.00	61.64	AAAA N
ATOM	12	CA	GLU	1	54.602	11.778	67.081	1.00	54.77	AAAA C
ATOM	13	N	ILE	2	53.608	13.860	66.375	1.00	37.66	AAAA N
ATOM	15	CA	ILE	2	52.768	14.699	65.604	1.00	40.87	AAAA C
ATOM	16	CB	ILE	2	52.925	16.122	66.160	1.00	41.97	AAAA C
ATOM	17	CG2	ILE	2	52.036	17.122	65.484	1.00	38.50	AAAA C
ATOM	18	CG1	ILE	2	52.560	16.006	67.663	1.00	46.58	AAAA C
ATOM	19	CD1	ILE	2	53.150	17.176	68.498	1.00	32.29	AAAA C
ATOM	20	C	ILE	2	53.122	14.711	64.139	1.00	46.47	AAAA C
ATOM	21	O	ILE	2	54.258	15.029	63.852	1.00	51.66	AAAA O
ATOM	22	N	CYS	3	52.235	14.409	63.196	1.00	49.61	AAAA N
ATOM	24	CA	CYS	3	52.435	14.677	61.773	1.00	38.93	AAAA C
ATOM	25	C	CYS	3	51.429	15.708	61.302	1.00	42.06	AAAA C
ATOM	26	O	CYS	3	50.290	15.521	61.690	1.00	42.37	AAAA O
ATOM	27	CB	CYS	3	52.159	13.415	60.999	1.00	35.66	AAAA C
ATOM	28	SG	CYS	3	53.019	12.004	61.674	1.00	36.98	AAAA S
ATOM	29	N	GLY	4	51.851	16.709	60.580	1.00	42.39	AAAA N
ATOM	31	CA	GLY	4	50.973	17.718	60.003	1.00	47.71	AAAA C
ATOM	32	C	GLY	4	51.703	18.407	58.869	1.00	48.23	AAAA C
ATOM	33	O	GLY	4	52.916	18.345	58.884	1.00	55.36	AAAA O
ATOM	34	N	PRO	5	51.056	19.212	58.048	1.00	49.63	AAAA N
ATOM	35	CD	PRO	5	51.637	19.947	56.860	1.00	45.28	AAAA C
ATOM	36	CA	PRO	5	49.605	19.341	58.083	1.00	41.57	AAAA C
ATOM	37	CB	PRO	5	49.397	20.703	57.474	1.00	44.30	AAAA C
ATOM	38	CG	PRO	5	50.632	21.036	56.683	1.00	46.43	AAAA C
ATOM	39	C	PRO	5	48.932	18.217	57.354	1.00	36.40	AAAA C
ATOM	40	O	PRO	5	49.403	17.094	57.396	1.00	43.35	AAAA O
ATOM	41	N	GLY	6	47.787	18.438	56.795	1.00	39.15	AAAA N
ATOM	43	CA	GLY	6	46.896	17.336	56.350	1.00	39.24	AAAA C
ATOM	44	C	GLY	6	47.710	16.365	55.529	1.00	33.68	AAAA C
ATOM	45	O	GLY	6	48.510	16.863	54.753	1.00	36.00	AAAA O
ATOM	46	N	ILE	7	47.586	15.111	55.788	1.00	35.70	AAAA N
ATOM	48	CA	ILE	7	48.307	14.053	55.141	1.00	37.65	AAAA C
ATOM	49	CB	ILE	7	48.556	12.797	55.933	1.00	36.31	AAAA C
ATOM	50	CG2	ILE	7	49.043	11.700	54.988	1.00	34.67	AAAA C
ATOM	51	CG1	ILE	7	49.561	12.857	57.067	1.00	39.34	AAAA C
ATOM	52	CD1	ILE	7	49.678	14.249	57.668	1.00	40.22	AAAA C
ATOM	53	C	ILE	7	47.338	13.762	53.977	1.00	45.00	AAAA C
ATOM	54	O	ILE	7	46.150	13.843	54.195	1.00	51.52	AAAA O
ATOM	55	N	ASP	8	47.767	13.631	52.751	1.00	45.60	AAAA N
ATOM	57	CA	ASP	8	46.938	13.283	51.631	1.00	44.05	AAAA C
ATOM	58	CB	ASP	8	47.003	14.469	50.651	1.00	44.21	AAAA C
ATOM	59	CG	ASP	8	45.909	14.379	49.600	1.00	43.48	AAAA C
ATOM	60	OD1	ASP	8	45.660	13.262	49.096	1.00	51.77	AAAA O
ATOM	61	OD2	ASP	8	45.253	15.374	49.251	1.00	46.84	AAAA O
ATOM	62	C	ASP	8	47.428	12.000	50.992	1.00	42.16	AAAA C
ATOM	63	O	ASP	8	48.423	12.143	50.330	1.00	48.50	AAAA O
ATOM	64	N	ILE	9	47.096	10.817	51.321	1.00	42.76	AAAA N
ATOM	66	CA	ILE	9	47.441	9.505	50.939	1.00	44.05	AAAA C
ATOM	67	CB	ILE	9	47.212	8.483	52.077	1.00	40.82	AAAA C
ATOM	68	CG2	ILE	9	47.669	7.085	51.653	1.00	36.35	AAAA C
ATOM	69	CG1	ILE	9	47.888	8.917	53.364	1.00	41.17	AAAA C
ATOM	70	CD1	ILE	9	49.376	8.947	53.286	1.00	43.78	AAAA C
ATOM	71	C	ILE	9	46.530	9.137	49.794	1.00	51.48	AAAA C
ATOM	72	O	ILE	9	45.338	9.420	49.832	1.00	63.05	AAAA O
ATOM	73	N	ARG	10	47.004	8.417	48.812	1.00	54.87	AAAA N
ATOM	75	CA	ARG	10	46.283	8.089	47.600	1.00	54.17	AAAA C
ATOM	76	CB	ARG	10	45.703	9.358	47.023	1.00	48.54	AAAA C
ATOM	77	CG	ARG	10	46.361	10.169	45.952	1.00	46.55	AAAA C
ATOM	78	CD	ARG	10	46.002	11.635	46.264	1.00	52.63	AAAA C
ATOM	79	NE	ARG	10	45.082	12.226	45.284	1.00	59.27	AAAA N
ATOM	81	CZ	ARG	10	44.269	13.262	45.498	1.00	56.22	AAAA C
ATOM	82	NH1	ARG	10	44.153	13.891	46.666	1.00	55.14	AAAA N
ATOM	85	NH2	ARG	10	43.455	13.803	44.602	1.00	52.29	AAAA N
ATOM	88	C	ARG	10	47.019	7.373	46.492	1.00	57.23	AAAA C
ATOM	89	O	ARG	10	48.240	7.288	46.281	1.00	56.32	AAAA O
ATOM	90	N	ASN	11	46.248	6.654	45.629	1.00	57.23	AAAA N
ATOM	92	CA	ASN	11	46.800	5.917	44.494	1.00	50.73	AAAA C
ATOM	93	CB	ASN	11	47.704	6.798	43.671	1.00	44.65	AAAA C
ATOM	94	CG	ASN	11	46.878	7.732	42.829	1.00	50.72	AAAA C
ATOM	95	OD1	ASN	11	45.749	7.451	42.403	1.00	72.59	AAAA O
ATOM	96	ND2	ASN	11	47.499	8.869	42.587	1.00	54.38	AAAA N
ATOM	99	C	ASN	11	47.635	4.736	44.915	1.00	53.07	AAAA C
ATOM	100	O	ASN	11	47.303	3.701	44.347	1.00	51.95	AAAA O
ATOM	101	N	ASP	12	48.566	4.822	45.878	1.00	50.96	AAAA N
ATOM	103	CA	ASP	12	49.204	3.570	46.263	1.00	55.44	AAAA C

ATOM	104	CB	ASP	12	50.669	3.568	45.758	1.00	66.47	AAAA C
ATOM	105	CG	ASP	12	50.879	4.026	44.314	1.00	68.25	AAAA C
ATOM	106	OD1	ASP	12	50.441	3.185	43.457	1.00	58.31	AAAA O
ATOM	107	OD2	ASP	12	51.391	5.120	43.989	1.00	70.56	AAAA O
ATOM	108	C	ASP	12	49.061	3.322	47.758	1.00	59.23	AAAA C
ATOM	109	O	ASP	12	49.687	3.849	48.711	1.00	59.65	AAAA O
ATOM	110	N	TYR	13	48.411	2.187	48.036	1.00	59.64	AAAA N
ATOM	112	CA	TYR	13	48.328	1.672	49.397	1.00	64.06	AAAA C
ATOM	113	CB	TYR	13	47.968	0.196	49.409	1.00	64.56	AAAA C
ATOM	114	CG	TYR	13	47.467	-0.357	50.721	1.00	69.18	AAAA C
ATOM	115	CD1	TYR	13	46.216	-0.024	51.248	1.00	72.71	AAAA C
ATOM	116	CE1	TYR	13	45.746	-0.541	52.450	1.00	71.51	AAAA C
ATOM	117	CD2	TYR	13	48.233	-1.247	51.457	1.00	70.36	AAAA C
ATOM	118	CE2	TYR	13	47.788	-1.778	52.661	1.00	71.64	AAAA C
ATOM	119	CZ	TYR	13	46.542	-1.420	53.160	1.00	71.31	AAAA C
ATOM	120	OH	TYR	13	46.144	-1.977	54.358	1.00	63.25	AAAA O
ATOM	122	C	TYR	13	49.622	1.839	50.198	1.00	65.99	AAAA C
ATOM	123	O	TYR	13	49.621	2.321	51.354	1.00	65.01	AAAA O
ATOM	124	N	GLN	14	50.786	1.541	49.594	1.00	63.51	AAAA N
ATOM	126	CA	GLN	14	52.078	1.681	50.218	1.00	63.51	AAAA C
ATOM	127	CB	GLN	14	53.174	1.318	49.219	1.00	68.37	AAAA C
ATOM	128	CG	GLN	14	52.863	-0.078	48.686	1.00	84.62	AAAA C
ATOM	129	CD	GLN	14	53.990	-0.515	47.754	1.00	92.28	AAAA C
ATOM	130	OE1	GLN	14	53.945	-0.161	46.573	1.00	94.82	AAAA O
ATOM	131	NE2	GLN	14	54.920	-1.254	48.361	1.00	98.03	AAAA N
ATOM	134	C	GLN	14	52.434	3.058	50.753	1.00	61.62	AAAA C
ATOM	135	O	GLN	14	53.266	3.292	51.644	1.00	62.09	AAAA O
ATOM	136	N	GLN	15	51.628	4.038	50.349	1.00	57.02	AAAA N
ATOM	138	CA	GLN	15	51.724	5.399	50.831	1.00	51.71	AAAA C
ATOM	139	CB	GLN	15	50.861	6.220	49.911	1.00	43.75	AAAA C
ATOM	140	CG	GLN	15	51.566	6.605	48.648	1.00	59.65	AAAA C
ATOM	141	CD	GLN	15	51.554	8.105	48.428	1.00	72.96	AAAA C
ATOM	142	OE1	GLN	15	51.168	9.005	49.184	1.00	80.58	AAAA O
ATOM	143	NE2	GLN	15	52.016	8.378	47.211	1.00	74.17	AAAA N
ATOM	146	C	GLN	15	51.219	5.530	52.258	1.00	50.15	AAAA C
ATOM	147	O	GLN	15	51.576	6.500	52.940	1.00	48.04	AAAA O
ATOM	148	N	LEU	16	50.440	4.535	52.688	1.00	46.22	AAAA N
ATOM	150	CA	LEU	16	49.913	4.449	54.019	1.00	45.52	AAAA C
ATOM	151	CB	LEU	16	48.950	3.295	54.159	1.00	37.73	AAAA C
ATOM	152	CG	LEU	16	47.502	3.425	53.707	1.00	41.40	AAAA C
ATOM	153	CD1	LEU	16	46.837	2.063	53.790	1.00	42.43	AAAA C
ATOM	154	CD2	LEU	16	46.687	4.424	54.545	1.00	35.93	AAAA C
ATOM	155	C	LEU	16	51.042	4.280	55.039	1.00	51.52	AAAA C
ATOM	156	O	LEU	16	50.913	4.601	56.235	1.00	52.53	AAAA O
ATOM	157	N	LYS	17	52.252	3.936	54.560	1.00	51.01	AAAA N
ATOM	159	CA	LYS	17	53.422	3.914	55.404	1.00	50.73	AAAA C
ATOM	160	CB	LYS	17	54.609	3.252	54.737	1.00	56.10	AAAA C
ATOM	161	CG	LYS	17	54.539	1.733	54.831	1.00	62.40	AAAA C
ATOM	162	CD	LYS	17	54.768	1.278	53.387	1.00	63.85	AAAA C
ATOM	163	CE	LYS	17	55.316	-0.141	53.426	1.00	68.40	AAAA C
ATOM	164	NZ	LYS	17	56.537	-0.225	52.554	1.00	73.83	AAAA N
ATOM	168	C	LYS	17	53.944	5.270	55.852	1.00	44.78	AAAA C
ATOM	169	O	LYS	17	54.492	5.262	56.933	1.00	39.39	AAAA O
ATOM	170	N	ARG	18	53.524	6.344	55.201	1.00	41.15	AAAA N
ATOM	172	CA	ARG	18	53.827	7.673	55.676	1.00	43.01	AAAA C
ATOM	173	CB	ARG	18	53.250	8.702	54.704	1.00	43.97	AAAA C
ATOM	174	CG	ARG	18	53.888	8.764	53.333	1.00	53.60	AAAA C
ATOM	175	CD	ARG	18	52.964	9.362	52.269	1.00	60.34	AAAA C
ATOM	176	NE	ARG	18	52.528	10.703	52.650	1.00	50.00	AAAA N
ATOM	178	CZ	ARG	18	51.628	11.444	52.021	1.00	48.86	AAAA C
ATOM	179	NH1	ARG	18	51.068	10.941	50.943	1.00	47.96	AAAA N
ATOM	182	NH2	ARG	18	51.377	12.656	52.555	1.00	43.72	AAAA N
ATOM	185	C	ARG	18	53.258	7.924	57.077	1.00	44.03	AAAA C
ATOM	186	O	ARG	18	53.402	9.010	57.644	1.00	45.53	AAAA O
ATOM	187	N	LEU	19	52.445	7.069	57.632	1.00	46.36	AAAA N
ATOM	189	CA	LEU	19	51.653	7.282	58.794	1.00	50.25	AAAA C
ATOM	190	CB	LEU	19	50.186	6.924	58.674	1.00	50.83	AAAA C
ATOM	191	CG	LEU	19	49.202	7.371	57.608	1.00	46.43	AAAA C
ATOM	192	CD1	LEU	19	47.946	6.743	57.852	1.00	22.57	AAAA C
ATOM	193	CD2	LEU	19	49.018	8.866	57.495	1.00	45.88	AAAA C
ATOM	194	C	LEU	19	52.210	6.428	59.912	1.00	49.87	AAAA C
ATOM	195	O	LEU	19	51.870	6.810	61.030	1.00	51.54	AAAA O
ATOM	196	N	GLU	20	53.270	5.708	59.652	1.00	49.35	AAAA N
ATOM	198	CA	GLU	20	53.819	4.833	60.679	1.00	49.60	AAAA C
ATOM	199	CB	GLU	20	54.876	3.960	59.982	1.00	57.91	AAAA C
ATOM	200	CG	GLU	20	55.893	4.840	59.272	1.00	70.16	AAAA C
ATOM	201	CD	GLU	20	57.095	4.077	58.757	1.00	69.35	AAAA C
ATOM	202	OE1	GLU	20	58.123	4.795	58.722	1.00	71.38	AAAA O
ATOM	203	OE2	GLU	20	56.993	2.885	58.420	1.00	72.84	AAAA O
ATOM	204	C	GLU	20	54.310	5.417	61.989	1.00	43.55	AAAA C
ATOM	205	O	GLU	20	54.301	4.652	62.937	1.00	40.01	AAAA O
ATOM	206	N	ASN	21	54.633	6.659	62.207	1.00	41.06	AAAA N
ATOM	208	CA	ASN	21	55.054	7.204	63.454	1.00	47.17	AAAA C
ATOM	209	C	ASN	21	54.066	8.141	64.108	1.00	49.76	AAAA C
ATOM	210	O	ASN	21	54.229	8.456	65.303	1.00	48.10	AAAA O

ATOM	211	CB	ASN	21	56.379	6.093	63.299	1.00	59.11	AAAA C
ATOM	212	CG	ASN	21	57.413	7.051	62.796	1.00	68.38	AAAA C
ATOM	213	OD1	ASN	21	57.499	5.855	63.122	1.00	58.51	AAAA O
ATOM	214	ND2	ASN	21	58.348	7.469	61.890	1.00	77.90	AAAA N
ATOM	216	N	CYS	22	53.129	8.711	63.351	1.00	47.44	AAAA N
ATOM	218	CA	CYS	22	52.107	9.614	63.879	1.00	42.99	AAAA C
ATOM	219	C	CYS	22	51.215	9.089	65.021	1.00	40.43	AAAA C
ATOM	220	O	CYS	22	50.750	7.923	65.069	1.00	36.07	AAAA O
ATOM	221	CB	CYS	22	51.182	9.921	62.690	1.00	44.82	AAAA C
ATOM	222	SG	CYS	22	52.076	10.328	61.148	1.00	39.51	AAAA S
ATOM	223	N	THR	23	51.287	9.801	66.137	1.00	36.24	AAAA N
ATOM	225	CA	THR	23	50.339	9.482	67.204	1.00	43.51	AAAA C
ATOM	226	CB	THR	23	50.944	9.481	68.593	1.00	41.38	AAAA C
ATOM	227	OG1	THR	23	51.410	10.843	68.822	1.00	51.21	AAAA O
ATOM	229	CG2	THR	23	52.110	8.571	68.838	1.00	33.83	AAAA C
ATOM	230	C	THR	23	49.250	10.599	67.116	1.00	44.55	AAAA C
ATOM	231	O	THR	23	48.085	10.414	67.481	1.00	45.95	AAAA O
ATOM	232	N	VAL	24	49.646	11.797	66.689	1.00	33.03	AAAA N
ATOM	234	CA	VAL	24	48.732	12.855	66.442	1.00	35.29	AAAA C
ATOM	235	CB	VAL	24	48.925	13.979	67.456	1.00	30.60	AAAA C
ATOM	236	CG1	VAL	24	48.056	15.157	67.082	1.00	27.21	AAAA C
ATOM	237	CG2	VAL	24	48.656	13.566	68.886	1.00	25.37	AAAA C
ATOM	238	C	VAL	24	48.895	13.447	65.043	1.00	41.52	AAAA C
ATOM	239	O	VAL	24	49.987	13.963	64.791	1.00	44.40	AAAA O
ATOM	240	N	ILE	25	47.855	13.450	64.203	1.00	40.13	AAAA N
ATOM	242	CA	ILE	25	47.908	14.094	62.882	1.00	32.05	AAAA C
ATOM	243	CB	ILE	25	47.113	13.299	61.853	1.00	25.85	AAAA C
ATOM	244	CG2	ILE	25	47.027	14.039	60.542	1.00	18.73	AAAA C
ATOM	245	CG1	ILE	25	47.677	11.896	61.705	1.00	29.80	AAAA C
ATOM	246	CD1	ILE	25	47.169	11.155	60.471	1.00	27.41	AAAA C
ATOM	247	C	ILE	25	47.397	15.490	62.941	1.00	32.92	AAAA C
ATOM	248	O	ILE	25	46.223	15.776	63.213	1.00	40.91	AAAA O
ATOM	249	N	GLU	26	48.264	16.472	63.042	1.00	36.60	AAAA N
ATOM	251	CA	GLU	26	47.832	17.847	63.226	1.00	29.24	AAAA C
ATOM	252	CB	GLU	26	48.875	18.703	63.856	1.00	29.92	AAAA C
ATOM	253	CG	GLU	26	48.490	20.144	64.116	1.00	38.06	AAAA C
ATOM	254	CD	GLU	26	49.561	20.762	65.013	1.00	37.39	AAAA C
ATOM	255	OE1	GLU	26	50.654	20.937	64.489	1.00	41.56	AAAA O
ATOM	256	OE2	GLU	26	49.571	21.175	66.182	1.00	49.16	AAAA O
ATOM	257	C	GLU	26	47.413	18.376	61.869	1.00	37.79	AAAA C
ATOM	258	O	GLU	26	48.161	19.069	61.181	1.00	39.68	AAAA O
ATOM	259	N	GLY	27	46.117	18.104	61.582	1.00	37.28	AAAA N
ATOM	261	CA	GLY	27	45.498	18.503	60.320	1.00	31.17	AAAA C
ATOM	262	C	GLY	27	44.531	17.400	59.893	1.00	33.72	AAAA C
ATOM	263	O	GLY	27	43.988	16.715	60.775	1.00	33.29	AAAA O
ATOM	264	N	TYR	28	44.304	17.209	58.604	1.00	29.24	AAAA N
ATOM	266	CA	TYR	28	43.318	16.189	58.253	1.00	28.93	AAAA C
ATOM	267	CB	TYR	28	42.403	16.794	57.217	1.00	31.53	AAAA C
ATOM	268	CG	TYR	28	43.058	17.256	55.962	1.00	31.78	AAAA C
ATOM	269	CD1	TYR	28	43.704	16.355	55.116	1.00	36.07	AAAA C
ATOM	270	CE1	TYR	28	44.361	16.706	53.967	1.00	28.91	AAAA C
ATOM	271	CD2	TYR	28	43.130	18.572	55.606	1.00	30.98	AAAA C
ATOM	272	CE2	TYR	28	43.769	18.972	54.428	1.00	28.77	AAAA C
ATOM	273	CZ	TYR	28	44.367	18.021	53.652	1.00	31.53	AAAA C
ATOM	274	OH	TYR	28	44.971	18.425	52.464	1.00	44.74	AAAA O
ATOM	276	C	TYR	28	43.953	14.946	57.697	1.00	29.23	AAAA C
ATOM	277	O	TYR	28	45.119	15.147	57.383	1.00	35.58	AAAA O
ATOM	278	N	LEU	29	43.250	13.900	57.445	1.00	26.63	AAAA N
ATOM	280	CA	LEU	29	43.764	12.730	56.803	1.00	29.83	AAAA C
ATOM	281	CB	LEU	29	43.830	11.611	57.856	1.00	27.09	AAAA C
ATOM	282	CG	LEU	29	44.212	10.258	57.242	1.00	31.90	AAAA C
ATOM	283	CD1	LEU	29	45.538	10.396	56.469	1.00	35.03	AAAA C
ATOM	284	CD2	LEU	29	44.551	9.203	58.290	1.00	25.05	AAAA C
ATOM	285	C	LEU	29	42.897	12.342	55.616	1.00	33.84	AAAA C
ATOM	286	O	LEU	29	41.689	12.165	55.806	1.00	43.29	AAAA O
ATOM	287	N	HIS	30	43.369	12.285	54.395	1.00	35.95	AAAA N
ATOM	289	CA	HIS	30	42.681	11.891	53.197	1.00	34.92	AAAA C
ATOM	290	CB	HIS	30	42.893	12.801	52.027	1.00	32.85	AAAA C
ATOM	291	CG	HIS	30	42.372	14.155	52.046	1.00	25.08	AAAA C
ATOM	292	CD2	HIS	30	41.519	14.753	52.907	1.00	40.88	AAAA C
ATOM	293	ND1	HIS	30	42.717	15.120	51.128	1.00	33.66	AAAA N
ATOM	295	CE1	HIS	30	42.080	16.281	51.444	1.00	31.33	AAAA C
ATOM	296	NE2	HIS	30	41.329	16.093	52.539	1.00	37.27	AAAA N
ATOM	298	C	HIS	30	43.173	10.538	52.714	1.00	37.68	AAAA C
ATOM	299	O	HIS	30	44.357	10.388	52.541	1.00	38.70	AAAA O
ATOM	300	N	ILE	31	42.308	9.542	52.584	1.00	40.02	AAAA N
ATOM	302	CA	ILE	31	42.750	8.271	51.992	1.00	39.47	AAAA C
ATOM	303	CB	ILE	31	42.668	7.204	53.063	1.00	37.95	AAAA C
ATOM	304	CG2	ILE	31	43.161	5.830	52.651	1.00	23.86	AAAA C
ATOM	305	CG1	ILE	31	43.481	7.555	54.335	1.00	41.66	AAAA C
ATOM	306	CD1	ILE	31	43.170	6.575	55.473	1.00	28.22	AAAA C
ATOM	307	C	ILE	31	41.884	8.044	50.755	1.00	46.52	AAAA C
ATOM	308	O	ILE	31	40.753	7.589	50.827	1.00	43.56	AAAA O
ATOM	309	N	LEU	32	42.314	8.489	49.556	1.00	49.89	AAAA N
ATOM	311	CA	LEU	32	41.484	8.235	48.380	1.00	49.77	AAAA C

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ATOM   312  CB  LEU  32      41.127   9.515  47.603  1.00 47.49      AAAA C
ATOM   313  CG  LEU  32      42.691  10.688  47.562  1.00 45.33      AAAA C
ATOM   314  CD1 LEU  32      41.517  11.812  46.673  1.00 35.77      AAAA C
ATOM   315  CD2 LEU  32      42.371  11.229  48.960  1.00 49.18      AAAA C
ATOM   316  C   LEU  32      42.136   7.296  47.353  1.00 51.00      AAAA C
ATOM   317  O   LEU  32      43.338   7.370  47.186  1.00 41.36      AAAA O
ATOM   318  N   LEU  33      41.270   6.722  46.497  1.00 50.74      AAAA N
ATOM   320  CA  LEU  33      41.602   6.175  45.197  1.00 49.92      AAAA C
ATOM   321  CB  LEU  33      42.091   7.262  44.182  1.00 34.83      AAAA C
ATOM   322  CG  LEU  33      41.233   8.537  44.164  1.00 33.92      AAAA C
ATOM   323  CD1 LEU  33      41.892   9.587  43.298  1.00 37.49      AAAA C
ATOM   324  CD2 LEU  33      39.823   8.313  43.644  1.00 33.01      AAAA C
ATOM   325  C   LEU  33      42.618   5.073  45.287  1.00 48.35      AAAA C
ATOM   326  O   LEU  33      43.580   5.077  44.538  1.00 54.14      AAAA O
ATOM   327  N   ILE  34      42.543   4.212  46.254  1.00 47.61      AAAA N
ATOM   329  CA  ILE  34      43.523   3.184  46.540  1.00 51.70      AAAA C
ATOM   330  CB  ILE  34      44.101   3.346  47.963  1.00 57.98      AAAA C
ATOM   331  CG2 ILE  34      44.538   2.043  48.600  1.00 48.98      AAAA C
ATOM   332  CG1 ILE  34      45.267   4.371  47.967  1.00 46.70      AAAA C
ATOM   333  CD1 ILE  34      45.561   4.704  49.439  1.00 66.47      AAAA C
ATOM   334  C   ILE  34      42.829   1.844  46.408  1.00 59.85      AAAA C
ATOM   335  O   ILE  34      41.726   1.531  46.856  1.00 60.11      AAAA O
ATOM   336  N   SER  35      43.622   0.833  46.013  1.00 67.79      AAAA N
ATOM   338  CA  SER  35      43.048  -0.511  45.922  1.00 68.80      AAAA C
ATOM   339  CB  SER  35      42.767  -0.882  44.469  1.00 64.16      AAAA C
ATOM   340  OG  SER  35      41.731  -1.846  44.498  1.00 75.76      AAAA O
ATOM   342  C   SER  35      43.928  -1.564  46.537  1.00 70.73      AAAA C
ATOM   343  O   SER  35      44.885  -1.954  45.909  1.00 73.65      AAAA O
ATOM   344  N   LYS  36      43.687  -2.017  47.740  1.00 74.75      AAAA N
ATOM   346  CA  LYS  36      44.465  -3.014  48.421  1.00 76.09      AAAA C
ATOM   347  CB  LYS  36      44.046  -3.131  49.885  1.00 81.22      AAAA C
ATOM   348  CG  LYS  36      45.147  -3.654  50.775  1.00 78.87      AAAA C
ATOM   349  CD  LYS  36      44.693  -4.575  51.887  1.00 81.39      AAAA C
ATOM   350  CE  LYS  36      44.899  -6.025  51.492  1.00 89.38      AAAA C
ATOM   351  NZ  LYS  36      44.371  -6.989  52.506  1.00 91.63      AAAA N
ATOM   355  C   LYS  36      44.252  -4.362  47.753  1.00 81.41      AAAA C
ATOM   356  O   LYS  36      43.145  -4.772  47.451  1.00 78.20      AAAA O
ATOM   357  N   ALA  37      45.371  -5.080  47.615  1.00 88.27      AAAA N
ATOM   359  CA  ALA  37      45.361  -6.396  46.986  1.00 90.10      AAAA C
ATOM   360  CB  ALA  37      46.700  -6.655  46.327  1.00 95.49      AAAA C
ATOM   361  C   ALA  37      45.011  -7.473  47.995  1.00 92.36      AAAA C
ATOM   362  O   ALA  37      45.668  -7.627  49.012  1.00 92.35      AAAA O
ATOM   363  N   SER  38      44.031  -8.301  47.622  1.00 94.31      AAAA N
ATOM   365  CA  SER  38      43.528  -9.352  48.484  1.00 95.70      AAAA C
ATOM   366  CB  SER  38      42.405 -10.164  47.858  1.00 97.44      AAAA C
ATOM   367  OG  SER  38      42.061 -11.176  48.814  1.00103.48      AAAA O
ATOM   369  C   SER  38      44.702 -10.263  48.821  1.00 96.87      AAAA C
ATOM   370  O   SER  38      44.761 -10.778  49.924  1.00 98.06      AAAA O
ATOM   371  N   ASP  39      45.584 -10.415  47.852  1.00 97.99      AAAA N
ATOM   373  CA  ASP  39      46.821 -11.148  47.980  1.00 99.19      AAAA C
ATOM   374  CB  ASP  39      47.579 -11.050  46.652  1.00102.13      AAAA C
ATOM   375  CG  ASP  39      47.696 -12.387  45.948  0.01101.22      AAAA C
ATOM   376  OD1 ASP  39      46.644 -12.978  45.623  0.01101.42      AAAA O
ATOM   377  OD2 ASP  39      48.833 -12.848  45.718  0.01101.41      AAAA O
ATOM   378  C   ASP  39      47.660 -10.564  49.105  1.00 99.40      AAAA C
ATOM   379  O   ASP  39      47.692 -11.056  50.224  1.00 99.15      AAAA O
ATOM   380  N   TYR  40      48.354  -9.479  48.818  1.00100.96      AAAA N
ATOM   382  CA  TYR  40      49.120  -8.706  49.802  1.00101.16      AAAA C
ATOM   383  CB  TYR  40      49.511  -7.393  49.130  1.00103.67      AAAA C
ATOM   384  CG  TYR  40      50.159  -6.281  49.887  1.00107.81      AAAA C
ATOM   385  CD1 TYR  40      50.931  -5.325  49.228  1.00109.56      AAAA C
ATOM   386  CE1 TYR  40      51.540  -4.280  49.910  1.00109.67      AAAA C
ATOM   387  CD2 TYR  40      50.044  -6.115  51.254  1.00109.28      AAAA C
ATOM   388  CE2 TYR  40      50.618  -5.102  51.976  1.00109.83      AAAA C
ATOM   389  CZ  TYR  40      51.372  -4.181  51.276  1.00110.16      AAAA C
ATOM   390  OH  TYR  40      51.999  -3.127  51.893  1.00109.84      AAAA O
ATOM   392  C   TYR  40      48.343  -8.529  51.100  1.00 99.19      AAAA C
ATOM   393  O   TYR  40      47.168  -8.182  51.183  1.00 99.05      AAAA O
ATOM   394  N   LYS  41      49.041  -8.653  52.218  1.00 98.62      AAAA N
ATOM   396  CA  LYS  41      48.443  -8.549  53.546  1.00100.30      AAAA C
ATOM   397  CB  LYS  41      49.385  -9.160  54.599  1.00104.42      AAAA C
ATOM   398  CG  LYS  41      49.218 -10.649  54.814  0.01101.06      AAAA C
ATOM   399  CD  LYS  41      47.776 -11.107  54.919  0.01100.66      AAAA C
ATOM   400  CE  LYS  41      47.205 -10.880  56.308  0.01 99.86      AAAA C
ATOM   401  NZ  LYS  41      47.882 -11.728  57.328  0.01 99.62      AAAA N
ATOM   405  C   LYS  41      48.035  -7.136  53.947  1.00 98.99      AAAA C
ATOM   406  O   LYS  41      47.615  -6.371  53.057  1.00103.33      AAAA O
ATOM   407  N   SER  42      48.198  -6.754  55.221  1.00 91.75      AAAA N
ATOM   409  CA  SER  42      47.825  -5.412  55.604  1.00 85.06      AAAA C
ATOM   410  CB  SER  42      46.385  -5.520  56.147  1.00 95.33      AAAA C
ATOM   411  OG  SER  42      46.547  -6.140  57.426  1.00104.63      AAAA O
ATOM   413  C   SER  42      48.628  -4.715  56.687  1.00 80.78      AAAA C
ATOM   414  O   SER  42      49.326  -5.259  57.538  1.00 81.03      AAAA O
ATOM   415  N   TYR  43      48.495  -3.395  56.673  1.00 73.03      AAAA N
ATOM   417  CA  TYR  43      49.069  -2.488  57.635  1.00 67.25      AAAA C
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ATOM	418	CB	TYR	43	49.096	-1.119	56.965	1.00	65.37	AAAA C
ATOM	419	CG	TYR	43	49.953	-1.021	55.727	1.00	63.92	AAAA C
ATOM	420	CD1	TYR	43	50.931	-1.935	55.406	1.00	63.87	AAAA C
ATOM	421	CE1	TYR	43	51.698	-1.781	54.274	1.00	66.09	AAAA C
ATOM	422	CD2	TYR	43	49.770	0.050	54.870	1.00	63.30	AAAA C
ATOM	423	CE2	TYR	43	50.536	0.214	53.728	1.00	67.62	AAAA C
ATOM	424	CZ	TYR	43	51.508	-0.712	53.432	1.00	66.94	AAAA C
ATOM	425	OH	TYR	43	52.262	-0.563	52.305	1.00	65.23	AAAA O
ATOM	427	C	TYR	43	48.248	-2.381	58.925	1.00	64.88	AAAA C
ATOM	428	O	TYR	43	47.088	-2.851	59.030	1.00	62.90	AAAA O
ATOM	429	N	ARG	44	48.782	-1.567	59.825	1.00	57.88	AAAA N
ATOM	431	CA	ARG	44	48.019	-1.285	61.039	1.00	56.45	AAAA C
ATOM	432	CB	ARG	44	47.842	-2.611	61.760	1.00	46.51	AAAA C
ATOM	433	CG	ARG	44	47.815	-2.375	63.244	1.00	54.66	AAAA C
ATOM	434	CD	ARG	44	46.885	-3.327	63.986	1.00	58.54	AAAA C
ATOM	435	NE	ARG	44	47.090	-2.927	65.403	1.00	68.56	AAAA N
ATOM	437	CZ	ARG	44	46.464	-3.536	66.395	1.00	64.82	AAAA C
ATOM	438	NH1	ARG	44	45.644	-4.529	66.132	1.00	61.53	AAAA N
ATOM	441	NH2	ARG	44	46.674	-3.139	67.628	1.00	66.03	AAAA N
ATOM	444	C	ARG	44	48.811	-0.285	61.845	1.00	55.59	AAAA C
ATOM	445	O	ARG	44	49.916	-0.552	62.320	1.00	58.43	AAAA O
ATOM	446	N	PHE	45	48.276	0.866	62.139	1.00	51.13	AAAA N
ATOM	448	CA	PHE	45	48.865	1.944	62.863	1.00	45.94	AAAA C
ATOM	449	CB	PHE	45	48.774	3.249	61.978	1.00	35.89	AAAA C
ATOM	450	CG	PHE	45	49.106	2.937	60.554	1.00	30.29	AAAA C
ATOM	451	CD1	PHE	45	50.373	3.051	59.998	1.00	45.72	AAAA C
ATOM	452	CD2	PHE	45	48.127	2.428	59.728	1.00	35.95	AAAA C
ATOM	453	CE1	PHE	45	50.653	2.715	58.672	1.00	47.76	AAAA C
ATOM	454	CE2	PHE	45	48.358	2.096	58.406	1.00	39.92	AAAA C
ATOM	455	CZ	PHE	45	49.612	2.244	57.967	1.00	46.44	AAAA C
ATOM	456	C	PHE	45	48.181	2.123	64.203	1.00	41.65	AAAA C
ATOM	457	O	PHE	45	47.708	3.223	64.475	1.00	40.99	AAAA O
ATOM	458	N	PRO	46	48.494	1.338	65.212	1.00	43.20	AAAA N
ATOM	459	CD	PRO	46	49.300	0.097	65.132	1.00	47.74	AAAA C
ATOM	460	CA	PRO	46	48.032	1.530	66.560	1.00	43.34	AAAA C
ATOM	461	CB	PRO	46	48.514	0.319	67.380	1.00	44.92	AAAA C
ATOM	462	CG	PRO	46	49.404	-0.464	66.514	1.00	45.48	AAAA C
ATOM	463	C	PRO	46	48.558	2.768	67.233	1.00	41.30	AAAA C
ATOM	464	O	PRO	46	48.329	2.830	68.443	1.00	44.57	AAAA O
ATOM	465	N	LYS	47	49.450	3.533	66.676	1.00	39.33	AAAA N
ATOM	467	CA	LYS	47	49.991	4.679	67.362	1.00	38.10	AAAA C
ATOM	468	CB	LYS	47	51.378	4.981	66.852	1.00	48.07	AAAA C
ATOM	469	CG	LYS	47	52.032	3.995	65.902	1.00	67.95	AAAA C
ATOM	470	CD	LYS	47	53.563	3.976	65.891	1.00	61.33	AAAA C
ATOM	471	CE	LYS	47	54.115	4.648	67.147	1.00	72.19	AAAA C
ATOM	472	NZ	LYS	47	54.024	6.132	66.874	1.00	79.29	AAAA N
ATOM	476	C	LYS	47	49.014	5.848	67.195	1.00	39.76	AAAA C
ATOM	477	O	LYS	47	49.189	6.827	67.952	1.00	35.45	AAAA O
ATOM	478	N	LEU	48	48.300	5.886	66.053	1.00	36.45	AAAA N
ATOM	480	CA	LEU	48	47.370	7.004	65.800	1.00	40.40	AAAA C
ATOM	481	CB	LEU	48	46.823	6.919	64.389	1.00	28.59	AAAA C
ATOM	482	CG	LEU	48	45.947	7.967	63.787	1.00	31.04	AAAA C
ATOM	483	CD1	LEU	48	46.637	9.310	63.878	1.00	36.86	AAAA C
ATOM	484	CD2	LEU	48	45.591	7.738	62.294	1.00	34.49	AAAA C
ATOM	485	C	LEU	48	46.186	7.022	66.807	1.00	42.21	AAAA C
ATOM	486	O	LEU	48	45.271	6.187	66.863	1.00	36.48	AAAA O
ATOM	487	N	THR	49	46.138	8.041	67.673	1.00	38.95	AAAA N
ATOM	489	CA	THR	49	45.045	8.151	68.574	1.00	37.96	AAAA C
ATOM	490	CB	THR	49	45.548	8.207	70.034	1.00	48.69	AAAA C
ATOM	491	OG1	THR	49	46.396	9.340	70.225	1.00	35.90	AAAA O
ATOM	493	CG2	THR	49	46.230	6.957	70.529	1.00	31.99	AAAA C
ATOM	494	C	THR	49	44.230	9.425	68.321	1.00	39.48	AAAA C
ATOM	495	O	THR	49	43.111	9.451	68.837	1.00	34.49	AAAA O
ATOM	496	N	VAL	50	44.735	10.415	67.605	1.00	37.32	AAAA N
ATOM	498	CA	VAL	50	43.995	11.664	67.418	1.00	38.72	AAAA C
ATOM	499	CB	VAL	50	44.293	12.708	68.503	1.00	37.24	AAAA C
ATOM	500	CG1	VAL	50	43.630	14.066	68.208	1.00	29.96	AAAA C
ATOM	501	CG2	VAL	50	43.884	12.311	69.913	1.00	32.52	AAAA C
ATOM	502	C	VAL	50	44.271	12.305	66.048	1.00	37.03	AAAA C
ATOM	503	O	VAL	50	45.195	11.863	65.431	1.00	37.96	AAAA O
ATOM	504	N	ILE	51	43.319	12.939	65.415	1.00	37.49	AAAA N
ATOM	506	CA	ILE	51	43.301	13.575	64.133	1.00	32.48	AAAA C
ATOM	507	CB	ILE	51	42.346	12.864	63.152	1.00	34.51	AAAA C
ATOM	508	CG2	ILE	51	41.995	13.802	61.978	1.00	32.31	AAAA C
ATOM	509	CG1	ILE	51	43.026	11.611	62.671	1.00	30.78	AAAA C
ATOM	510	CD1	ILE	51	42.358	10.559	61.815	1.00	19.69	AAAA C
ATOM	511	C	ILE	51	42.659	14.939	64.431	1.00	34.14	AAAA C
ATOM	512	O	ILE	51	41.546	14.830	64.923	1.00	29.08	AAAA O
ATOM	513	N	THR	52	43.342	16.058	64.238	1.00	33.93	AAAA N
ATOM	515	CA	THR	52	42.806	17.305	64.719	1.00	33.83	AAAA C
ATOM	516	CB	THR	52	43.961	18.338	64.939	1.00	35.39	AAAA C
ATOM	517	OG1	THR	52	44.726	18.567	63.781	1.00	41.28	AAAA O
ATOM	519	CG2	THR	52	44.775	17.926	66.154	1.00	22.01	AAAA C
ATOM	520	C	THR	52	41.741	17.961	63.863	1.00	39.02	AAAA C
ATOM	521	O	THR	52	41.202	19.030	64.243	1.00	38.88	AAAA O

ATOM	522	N	GLU	53	41.524	17.477	62.639	1.00 36.93	AAAA N
ATOM	524	CA	GLU	53	40.434	17.953	61.785	1.00 38.30	AAAA C
ATOM	525	CB	GLU	53	41.064	18.512	60.483	1.00 29.76	AAAA C
ATOM	526	CG	GLU	53	42.061	19.552	60.834	1.00 30.48	AAAA C
ATOM	527	CD	GLU	53	42.517	20.396	59.697	1.00 40.82	AAAA C
ATOM	528	OE1	GLU	53	42.638	19.908	58.556	1.00 57.56	AAAA O
ATOM	529	OE2	GLU	53	42.799	21.559	59.931	1.00 35.74	AAAA O
ATOM	530	C	GLU	53	39.506	16.789	61.388	1.00 39.19	AAAA C
ATOM	531	O	GLU	53	38.922	16.311	62.386	1.00 38.95	AAAA O
ATOM	532	N	TYR	54	39.539	16.353	60.102	1.00 30.60	AAAA N
ATOM	534	CA	TYR	54	38.666	15.342	59.713	1.00 35.96	AAAA C
ATOM	535	CB	TYR	54	37.654	15.802	58.636	1.00 30.71	AAAA C
ATOM	536	CG	TYR	54	38.247	16.476	57.388	1.00 21.18	AAAA C
ATOM	537	CD1	TYR	54	38.487	15.733	56.305	1.00 20.22	AAAA C
ATOM	538	CE1	TYR	54	38.980	16.243	55.086	1.00 21.04	AAAA C
ATOM	539	CD2	TYR	54	38.577	17.844	57.307	1.00 23.97	AAAA C
ATOM	540	CE2	TYR	54	39.049	18.384	56.124	1.00 24.69	AAAA C
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ATOM	542	OH	TYR	54	39.763	18.047	53.847	1.00 37.55	AAAA O
ATOM	544	C	TYR	54	39.405	14.115	59.142	1.00 33.87	AAAA C
ATOM	545	O	TYR	54	40.513	14.360	58.678	1.00 30.40	AAAA O
ATOM	546	N	LEU	55	38.683	13.021	59.004	1.00 23.24	AAAA N
ATOM	548	CA	LEU	55	39.111	11.812	58.454	1.00 30.08	AAAA C
ATOM	549	CB	LEU	55	39.011	10.663	59.510	1.00 14.78	AAAA C
ATOM	550	CG	LEU	55	39.349	9.314	58.818	1.00 26.98	AAAA C
ATOM	551	CD1	LEU	55	40.668	9.477	58.040	1.00 26.66	AAAA C
ATOM	552	CD2	LEU	55	39.496	8.093	59.705	1.00 14.45	AAAA C
ATOM	553	C	LEU	55	38.201	11.548	57.238	1.00 37.43	AAAA C
ATOM	554	O	LEU	55	36.995	11.632	57.427	1.00 39.55	AAAA O
ATOM	555	N	LEU	56	38.700	11.348	56.035	1.00 41.83	AAAA N
ATOM	557	CA	LEU	56	37.955	11.201	54.799	1.00 36.98	AAAA C
ATOM	558	CB	LEU	56	37.998	12.446	53.949	1.00 33.29	AAAA C
ATOM	559	CG	LEU	56	37.984	12.514	52.416	1.00 30.35	AAAA C
ATOM	560	CD1	LEU	56	37.076	11.460	51.821	1.00 47.95	AAAA C
ATOM	561	CD2	LEU	56	37.286	13.807	51.985	1.00 33.47	AAAA C
ATOM	562	C	LEU	56	38.595	10.047	54.008	1.00 39.75	AAAA C
ATOM	563	O	LEU	56	39.714	10.205	53.547	1.00 44.38	AAAA O
ATOM	564	N	LEU	57	37.846	9.008	53.800	1.00 36.68	AAAA N
ATOM	566	CA	LEU	57	38.133	7.832	53.034	1.00 41.53	AAAA C
ATOM	567	CB	LEU	57	37.944	6.588	53.916	1.00 37.00	AAAA C
ATOM	568	CG	LEU	57	39.064	6.534	55.026	1.00 36.13	AAAA C
ATOM	569	CD1	LEU	57	38.513	6.890	56.417	1.00 33.26	AAAA C
ATOM	570	CD2	LEU	57	39.630	5.162	55.039	1.00 24.11	AAAA C
ATOM	571	C	LEU	57	37.203	7.825	51.838	1.00 46.03	AAAA C
ATOM	572	O	LEU	57	35.985	7.993	51.969	1.00 44.78	AAAA O
ATOM	573	N	PHE	58	37.792	7.898	50.642	1.00 47.07	AAAA N
ATOM	575	CA	PHE	58	36.895	8.002	49.467	1.00 48.75	AAAA C
ATOM	576	CB	PHE	58	36.704	9.448	49.102	1.00 46.67	AAAA C
ATOM	577	CG	PHE	58	36.447	9.815	47.692	1.00 54.66	AAAA C
ATOM	578	CD1	PHE	58	37.413	9.706	46.697	1.00 55.19	AAAA C
ATOM	579	CD2	PHE	58	35.200	10.301	47.326	1.00 53.86	AAAA C
ATOM	580	CE1	PHE	58	37.124	10.063	45.396	1.00 50.36	AAAA C
ATOM	581	CE2	PHE	58	34.885	10.655	46.011	1.00 41.84	AAAA C
ATOM	582	CZ	PHE	58	35.877	10.521	45.037	1.00 46.50	AAAA C
ATOM	583	C	PHE	58	37.351	7.052	48.379	1.00 49.71	AAAA C
ATOM	584	O	PHE	58	38.487	7.073	47.934	1.00 52.16	AAAA O
ATOM	585	N	ARG	59	36.471	6.118	47.944	1.00 44.26	AAAA N
ATOM	587	CA	ARG	59	36.753	5.281	46.815	1.00 40.80	AAAA C
ATOM	588	CB	ARG	59	36.911	5.993	45.427	1.00 23.79	AAAA C
ATOM	589	CG	ARG	59	35.869	7.020	45.121	1.00 46.53	AAAA C
ATOM	590	CD	ARG	59	35.921	7.562	43.706	1.00 37.64	AAAA C
ATOM	591	NE	ARG	59	35.822	6.422	42.806	1.00 49.23	AAAA N
ATOM	593	CZ	ARG	59	34.950	5.832	42.036	1.00 41.36	AAAA C
ATOM	594	NH1	ARG	59	33.702	6.277	41.931	1.00 47.00	AAAA N
ATOM	597	NH2	ARG	59	35.237	4.729	41.327	1.00 42.58	AAAA N
ATOM	600	C	ARG	59	38.037	4.494	47.049	1.00 42.25	AAAA C
ATOM	601	O	ARG	59	38.981	4.513	46.232	1.00 44.11	AAAA O
ATOM	602	N	VAL	60	38.001	3.625	48.023	1.00 40.84	AAAA N
ATOM	604	CA	VAL	60	39.101	2.743	48.341	1.00 39.14	AAAA C
ATOM	605	CB	VAL	60	39.624	3.066	49.751	1.00 40.12	AAAA C
ATOM	606	CG1	VAL	60	40.407	1.872	50.296	1.00 35.05	AAAA C
ATOM	607	CG2	VAL	60	40.425	4.352	49.893	1.00 28.86	AAAA C
ATOM	608	C	VAL	60	38.539	1.337	48.368	1.00 43.56	AAAA C
ATOM	609	O	VAL	60	37.535	1.224	49.072	1.00 47.66	AAAA O
ATOM	610	N	ALA	61	39.094	0.371	47.659	1.00 41.92	AAAA N
ATOM	612	CA	ALA	61	38.617	-0.992	47.749	1.00 42.05	AAAA C
ATOM	613	CB	ALA	61	38.302	-1.483	46.364	1.00 52.40	AAAA C
ATOM	614	C	ALA	61	39.613	-1.934	48.386	1.00 43.08	AAAA C
ATOM	615	O	ALA	61	40.757	-1.602	48.670	1.00 50.59	AAAA O
ATOM	616	N	GLY	62	39.200	-3.105	48.849	1.00 45.71	AAAA N
ATOM	618	CA	GLY	62	40.136	-4.079	49.385	1.00 45.39	AAAA C
ATOM	619	C	GLY	62	40.262	-3.902	50.872	1.00 48.04	AAAA C
ATOM	620	O	GLY	62	40.587	-4.835	51.604	1.00 52.34	AAAA O
ATOM	621	N	LEU	63	39.985	-2.734	51.383	1.00 46.90	AAAA N
ATOM	623	CA	LEU	63	40.003	-2.443	52.805	1.00 49.11	AAAA C

ATOM	624	CB	LEU	63	40.274	-0.953	53.027	1.00	41.41	AAAA C
ATOM	625	CG	LEU	63	40.265	-0.423	54.443	1.00	53.41	AAAA C
ATOM	626	CD1	LEU	63	41.172	-1.164	55.416	1.00	48.27	AAAA C
ATOM	627	CD2	LEU	63	40.637	1.047	54.246	1.00	50.51	AAAA C
ATOM	628	C	LEU	63	38.643	-2.881	53.323	1.00	54.20	AAAA C
ATOM	629	O	LEU	63	37.587	-2.430	52.837	1.00	57.73	AAAA O
ATOM	630	N	GLU	64	38.658	-3.862	54.190	1.00	53.97	AAAA N
ATOM	632	CA	GLU	64	37.462	-4.448	54.749	1.00	56.96	AAAA C
ATOM	633	CB	GLU	64	37.689	-5.956	54.734	1.00	65.33	AAAA C
ATOM	634	CG	GLU	64	37.832	-6.484	53.293	1.00	75.14	AAAA C
ATOM	635	CD	GLU	64	37.104	-7.940	53.128	1.00	78.10	AAAA C
ATOM	636	OE1	GLU	64	37.424	-8.698	54.132	1.00	63.93	AAAA O
ATOM	637	OE2	GLU	64	37.036	-8.320	51.978	1.00	88.77	AAAA O
ATOM	638	C	GLU	64	37.096	-4.007	56.163	1.00	57.12	AAAA C
ATOM	639	O	GLU	64	35.986	-4.332	56.600	1.00	59.82	AAAA O
ATOM	640	N	SER	65	37.766	-3.042	56.761	1.00	50.64	AAAA N
ATOM	642	CA	SER	65	37.539	-2.523	58.060	1.00	47.19	AAAA C
ATOM	643	CB	SER	65	37.743	-3.596	59.139	1.00	49.24	AAAA C
ATOM	644	OG	SER	65	37.501	-2.971	60.429	1.00	50.90	AAAA O
ATOM	646	C	SER	65	38.516	-1.405	58.432	1.00	48.35	AAAA C
ATOM	647	O	SER	65	39.716	-1.692	58.374	1.00	52.75	AAAA O
ATOM	648	N	LEU	66	38.054	-0.289	58.984	1.00	41.03	AAAA N
ATOM	650	CA	LEU	66	38.956	0.758	59.405	1.00	41.94	AAAA C
ATOM	651	CB	LEU	66	38.247	2.083	59.498	1.00	25.25	AAAA C
ATOM	652	CG	LEU	66	37.283	2.476	58.402	1.00	34.49	AAAA C
ATOM	653	CD1	LEU	66	36.974	3.951	58.512	1.00	30.81	AAAA C
ATOM	654	CD2	LEU	66	37.767	2.200	56.994	1.00	34.34	AAAA C
ATOM	655	C	LEU	66	39.646	0.462	60.734	1.00	45.39	AAAA C
ATOM	656	O	LEU	66	40.762	0.947	60.927	1.00	41.05	AAAA O
ATOM	657	N	GLY	67	39.000	-0.346	61.583	1.00	45.21	AAAA N
ATOM	659	CA	GLY	67	39.773	-0.672	62.799	1.00	48.14	AAAA C
ATOM	660	C	GLY	67	40.998	-1.508	62.445	1.00	44.51	AAAA C
ATOM	661	O	GLY	67	41.855	-1.724	63.287	1.00	45.42	AAAA O
ATOM	662	N	ASP	68	41.013	-2.189	61.309	1.00	47.60	AAAA N
ATOM	664	CA	ASP	68	42.194	-2.834	60.738	1.00	50.99	AAAA C
ATOM	665	CB	ASP	68	42.012	-3.417	59.361	1.00	39.43	AAAA C
ATOM	666	CG	ASP	68	41.205	-4.678	59.311	1.00	45.82	AAAA C
ATOM	667	OD1	ASP	68	40.912	-5.341	60.320	1.00	44.69	AAAA O
ATOM	668	OD2	ASP	68	40.819	-5.065	58.187	1.00	47.23	AAAA O
ATOM	669	C	ASP	68	43.363	-1.837	60.596	1.00	45.89	AAAA C
ATOM	670	O	ASP	68	44.436	-2.269	60.903	1.00	44.84	AAAA O
ATOM	671	N	LEU	69	43.145	-0.609	60.247	1.00	42.49	AAAA N
ATOM	673	CA	LEU	69	44.175	0.352	60.048	1.00	45.80	AAAA C
ATOM	674	CB	LEU	69	43.920	1.393	58.945	1.00	45.25	AAAA C
ATOM	675	CG	LEU	69	43.902	0.882	57.494	1.00	54.25	AAAA C
ATOM	676	CD1	LEU	69	43.541	2.037	56.565	1.00	47.26	AAAA C
ATOM	677	CD2	LEU	69	45.211	0.200	57.113	1.00	50.76	AAAA C
ATOM	678	C	LEU	69	44.347	1.107	61.350	1.00	49.50	AAAA C
ATOM	679	O	LEU	69	45.470	1.210	61.851	1.00	54.51	AAAA O
ATOM	680	N	PHE	70	43.296	1.737	61.869	1.00	44.60	AAAA N
ATOM	682	CA	PHE	70	43.423	2.564	63.046	1.00	39.67	AAAA C
ATOM	683	CB	PHE	70	42.987	3.973	62.700	1.00	26.08	AAAA C
ATOM	684	CG	PHE	70	43.465	4.501	61.390	1.00	45.32	AAAA C
ATOM	685	CD1	PHE	70	42.532	4.748	60.384	1.00	47.41	AAAA C
ATOM	686	CD2	PHE	70	44.815	4.767	61.130	1.00	48.77	AAAA C
ATOM	687	CE1	PHE	70	42.945	5.263	59.159	1.00	56.16	AAAA C
ATOM	688	CE2	PHE	70	45.229	5.256	59.895	1.00	47.24	AAAA C
ATOM	689	CZ	PHE	70	44.293	5.506	58.896	1.00	49.54	AAAA C
ATOM	690	C	PHE	70	42.655	1.999	64.219	1.00	40.09	AAAA C
ATOM	691	O	PHE	70	41.874	2.734	64.838	1.00	35.74	AAAA O
ATOM	692	N	PRO	71	43.053	0.852	64.768	1.00	39.19	AAAA N
ATOM	693	CD	PRO	71	44.269	0.058	64.411	1.00	39.94	AAAA C
ATOM	694	CA	PRO	71	42.444	0.237	65.899	1.00	35.30	AAAA C
ATOM	695	CB	PRO	71	43.308	-0.983	66.246	1.00	38.03	AAAA C
ATOM	696	CG	PRO	71	44.669	-0.564	65.717	1.00	38.36	AAAA C
ATOM	697	C	PRO	71	42.453	1.089	67.126	1.00	33.72	AAAA C
ATOM	698	O	PRO	71	42.005	0.630	68.159	1.00	39.32	AAAA O
ATOM	699	N	ASN	72	43.058	2.220	67.231	1.00	36.55	AAAA N
ATOM	701	CA	ASN	72	43.204	3.032	68.401	1.00	32.60	AAAA C
ATOM	702	CB	ASN	72	44.637	2.916	68.962	1.00	36.89	AAAA C
ATOM	703	CG	ASN	72	44.735	1.638	69.761	1.00	47.03	AAAA C
ATOM	704	OD1	ASN	72	44.644	1.619	70.979	1.00	64.42	AAAA O
ATOM	705	ND2	ASN	72	44.880	0.475	69.169	1.00	63.17	AAAA N
ATOM	708	C	ASN	72	42.875	4.477	68.135	1.00	30.11	AAAA C
ATOM	709	O	ASN	72	43.099	5.201	69.104	1.00	36.53	AAAA O
ATOM	710	N	LEU	73	42.309	4.809	66.978	1.00	27.62	AAAA N
ATOM	712	CA	LEU	73	41.940	6.207	66.730	1.00	34.07	AAAA C
ATOM	713	CB	LEU	73	41.476	6.373	65.292	1.00	28.37	AAAA C
ATOM	714	CG	LEU	73	40.819	7.713	64.882	1.00	29.33	AAAA C
ATOM	715	CD1	LEU	73	41.918	8.721	64.963	1.00	31.86	AAAA C
ATOM	716	CD2	LEU	73	40.202	7.518	63.478	1.00	32.07	AAAA C
ATOM	717	C	LEU	73	40.929	6.569	67.817	1.00	32.14	AAAA C
ATOM	718	O	LEU	73	40.073	5.737	68.081	1.00	35.02	AAAA O
ATOM	719	N	THR	74	41.081	7.585	68.582	1.00	29.47	AAAA N
ATOM	721	CA	THR	74	40.150	7.826	69.683	1.00	34.80	AAAA C

ATOM	722	CB	THR	74	41.028	7.744	70.952	1.00	46.09	AAAA C
ATOM	723	OG1	THR	74	41.729	6.485	70.880	1.00	46.30	AAAA O
ATOM	725	CG2	THR	74	40.262	7.831	72.253	1.00	39.45	AAAA C
ATOM	726	C	THR	74	39.424	9.155	69.602	1.00	35.48	AAAA C
ATOM	727	O	THR	74	38.270	9.322	70.077	1.00	35.32	AAAA O
ATOM	728	N	VAL	75	40.047	10.198	69.073	1.00	29.80	AAAA N
ATOM	730	CA	VAL	75	39.351	11.474	68.892	1.00	34.91	AAAA C
ATOM	731	CB	VAL	75	39.856	12.445	69.955	1.00	26.03	AAAA C
ATOM	732	CG1	VAL	75	39.173	13.801	69.934	1.00	24.51	AAAA C
ATOM	733	CG2	VAL	75	39.675	11.910	71.366	1.00	19.87	AAAA C
ATOM	734	C	VAL	75	39.613	12.045	67.494	1.00	37.57	AAAA C
ATOM	735	O	VAL	75	40.724	11.808	67.022	1.00	35.99	AAAA O
ATOM	736	N	ILE	76	38.600	12.555	66.796	1.00	35.91	AAAA N
ATOM	738	CA	ILE	76	38.696	13.340	65.592	1.00	31.48	AAAA C
ATOM	739	CB	ILE	76	37.831	12.769	64.492	1.00	29.60	AAAA C
ATOM	740	CG2	ILE	76	37.856	13.630	63.208	1.00	19.54	AAAA C
ATOM	741	CG1	ILE	76	38.222	11.314	64.277	1.00	28.52	AAAA C
ATOM	742	CD1	ILE	76	37.149	10.556	63.478	1.00	28.85	AAAA C
ATOM	743	C	ILE	76	38.157	14.718	66.000	1.00	33.84	AAAA C
ATOM	744	O	ILE	76	36.987	14.777	66.274	1.00	38.84	AAAA O
ATOM	745	N	ARG	77	38.906	15.733	66.230	1.00	30.32	AAAA N
ATOM	747	CA	ARG	77	38.605	16.901	67.021	1.00	30.82	AAAA C
ATOM	748	CB	ARG	77	39.961	17.475	67.461	1.00	26.62	AAAA C
ATOM	749	CG	ARG	77	39.993	18.836	68.058	1.00	52.42	AAAA C
ATOM	750	CD	ARG	77	41.290	18.957	68.908	1.00	49.10	AAAA C
ATOM	751	NE	ARG	77	41.411	17.817	69.773	1.00	39.23	AAAA N
ATOM	753	CZ	ARG	77	40.977	18.016	71.064	1.00	48.79	AAAA C
ATOM	754	NH1	ARG	77	40.440	19.104	71.610	1.00	30.34	AAAA N
ATOM	757	NH2	ARG	77	41.061	17.012	71.941	1.00	40.38	AAAA N
ATOM	760	C	ARG	77	37.643	17.733	66.225	1.00	31.75	AAAA C
ATOM	761	O	ARG	77	36.944	18.637	66.664	1.00	31.40	AAAA O
ATOM	762	N	GLY	78	37.688	17.661	64.884	1.00	32.87	AAAA N
ATOM	764	CA	GLY	78	36.982	18.409	63.950	1.00	16.23	AAAA C
ATOM	765	C	GLY	78	37.199	19.880	64.063	1.00	31.58	AAAA C
ATOM	766	O	GLY	78	36.363	20.775	63.674	1.00	34.03	AAAA O
ATOM	767	N	TRP	79	38.439	20.321	64.304	1.00	31.21	AAAA N
ATOM	769	CA	TRP	79	38.757	21.740	64.337	1.00	30.80	AAAA C
ATOM	770	CB	TRP	79	40.177	21.943	64.845	1.00	39.07	AAAA C
ATOM	771	CG	TRP	79	40.626	23.343	65.164	1.00	36.64	AAAA C
ATOM	772	CD2	TRP	79	41.691	24.001	64.433	1.00	28.52	AAAA C
ATOM	773	CE2	TRP	79	41.826	25.288	65.002	1.00	36.49	AAAA C
ATOM	774	CE3	TRP	79	42.473	23.625	63.370	1.00	37.96	AAAA C
ATOM	775	CD1	TRP	79	40.199	24.235	66.113	1.00	29.59	AAAA C
ATOM	776	NE1	TRP	79	40.917	25.413	66.054	1.00	27.67	AAAA N
ATOM	778	CZ2	TRP	79	42.770	26.213	64.543	1.00	31.83	AAAA C
ATOM	779	CZ3	TRP	79	43.389	24.548	62.876	1.00	46.14	AAAA C
ATOM	780	CH2	TRP	79	43.525	25.794	63.470	1.00	35.31	AAAA C
ATOM	781	C	TRP	79	38.606	22.418	62.986	1.00	28.75	AAAA C
ATOM	782	O	TRP	79	38.585	23.624	62.961	1.00	23.61	AAAA O
ATOM	783	N	LYS	80	38.659	21.684	61.895	1.00	31.84	AAAA N
ATOM	785	CA	LYS	80	38.305	22.153	60.573	1.00	32.78	AAAA C
ATOM	786	CB	LYS	80	39.453	22.498	59.689	1.00	41.17	AAAA C
ATOM	787	CG	LYS	80	39.838	23.911	59.470	1.00	34.68	AAAA C
ATOM	788	CD	LYS	80	41.025	24.350	60.306	1.00	44.77	AAAA C
ATOM	789	CE	LYS	80	41.276	25.811	59.898	1.00	50.41	AAAA C
ATOM	790	NZ	LYS	80	42.530	25.752	59.092	1.00	67.26	AAAA N
ATOM	791	C	LYS	80	37.585	20.960	59.917	1.00	34.52	AAAA C
ATOM	792	O	LYS	80	37.950	19.843	60.237	1.00	37.62	AAAA O
ATOM	793	N	LEU	81	36.477	21.267	59.207	1.00	31.77	AAAA N
ATOM	795	CA	LEU	81	35.742	20.157	58.600	1.00	31.02	AAAA C
ATOM	796	CB	LEU	81	34.290	20.315	59.092	1.00	31.20	AAAA C
ATOM	797	CG	LEU	81	34.115	20.319	60.632	1.00	36.97	AAAA C
ATOM	798	CD1	LEU	81	32.832	21.080	60.954	1.00	27.98	AAAA C
ATOM	799	CD2	LEU	81	34.089	18.955	61.297	1.00	28.77	AAAA C
ATOM	800	C	LEU	81	35.733	20.023	57.104	1.00	29.86	AAAA C
ATOM	801	O	LEU	81	36.082	20.947	56.368	1.00	29.34	AAAA O
ATOM	802	N	PHE	82	35.430	18.813	56.594	1.00	27.78	AAAA N
ATOM	804	CA	PHE	82	35.176	18.653	55.182	1.00	28.68	AAAA C
ATOM	805	CB	PHE	82	35.513	17.226	54.795	1.00	32.78	AAAA C
ATOM	806	CG	PHE	82	35.348	16.901	53.357	1.00	30.48	AAAA C
ATOM	807	CD1	PHE	82	36.378	17.130	52.447	1.00	32.86	AAAA C
ATOM	808	CD2	PHE	82	34.142	16.361	52.914	1.00	30.93	AAAA C
ATOM	809	CE1	PHE	82	36.217	16.769	51.104	1.00	43.27	AAAA C
ATOM	810	CE2	PHE	82	33.963	16.061	51.538	1.00	26.30	AAAA C
ATOM	811	CZ	PHE	82	35.005	16.238	50.672	1.00	37.73	AAAA C
ATOM	812	C	PHE	82	33.670	18.911	54.993	1.00	30.06	AAAA C
ATOM	813	O	PHE	82	32.830	18.045	55.278	1.00	27.36	AAAA O
ATOM	814	N	TYR	83	33.301	20.148	54.770	1.00	31.68	AAAA N
ATOM	815	CA	TYR	83	31.911	20.605	54.633	1.00	40.76	AAAA C
ATOM	816	C	TYR	83	31.043	19.977	55.726	1.00	44.00	AAAA C
ATOM	817	O	TYR	83	30.075	19.210	55.487	1.00	50.47	AAAA O
ATOM	818	CB	TYR	83	31.359	20.199	53.269	1.00	31.55	AAAA C
ATOM	819	CG	TYR	83	32.196	20.742	52.115	0.01	20.00	AAAA C
ATOM	820	CD1	TYR	83	33.254	19.982	51.609	0.01	20.00	AAAA C
ATOM	821	CD2	TYR	83	31.906	21.998	51.575	0.01	20.00	AAAA C

ATOM	822	CE1	TYR	83	34.027	20.480	50.556	0.01	20.00	AAAA C
ATOM	823	CE2	TYR	83	32.679	22.496	50.521	0.01	20.00	AAAA C
ATOM	824	CZ	TYR	83	33.740	21.737	50.012	0.01	20.00	AAAA C
ATOM	825	OH	TYR	83	34.492	22.222	48.989	0.01	20.00	AAAA O
ATOM	826	N	ASN	84	31.043	20.461	56.924	1.00	40.91	AAAA N
ATOM	827	CA	ASN	84	30.250	20.057	58.056	1.00	36.54	AAAA C
ATOM	828	CB	ASN	84	28.763	20.046	57.700	1.00	47.84	AAAA C
ATOM	829	CG	ASN	84	28.274	21.164	56.797	1.00	60.75	AAAA C
ATOM	830	OD1	ASN	84	28.319	22.343	57.119	1.00	45.55	AAAA O
ATOM	831	ND2	ASN	84	27.839	20.876	55.552	1.00	65.98	AAAA N
ATOM	832	C	ASN	84	30.686	18.679	58.556	1.00	36.33	AAAA C
ATOM	833	O	ASN	84	30.137	18.206	59.580	1.00	38.24	AAAA O
ATOM	834	N	TYR	85	31.455	17.900	57.800	1.00	32.78	AAAA N
ATOM	836	CA	TYR	85	31.617	16.504	58.222	1.00	35.45	AAAA C
ATOM	837	CB	TYR	85	31.473	15.579	57.000	1.00	35.54	AAAA C
ATOM	838	CG	TYR	85	30.078	15.733	56.453	1.00	41.35	AAAA C
ATOM	839	CD1	TYR	85	29.868	16.291	55.199	1.00	38.22	AAAA C
ATOM	840	CE1	TYR	85	28.611	16.445	54.704	1.00	40.83	AAAA C
ATOM	841	CD2	TYR	85	28.954	15.371	57.200	1.00	47.42	AAAA C
ATOM	842	CE2	TYR	85	27.661	15.533	56.705	1.00	45.91	AAAA C
ATOM	843	CZ	TYR	85	27.497	16.072	55.445	1.00	46.06	AAAA C
ATOM	844	OH	TYR	85	26.258	16.315	54.886	1.00	46.05	AAAA O
ATOM	846	C	TYR	85	32.977	16.367	58.891	1.00	32.08	AAAA C
ATOM	847	O	TYR	85	33.943	16.977	58.405	1.00	37.44	AAAA O
ATOM	848	N	ALA	86	33.027	15.691	59.979	1.00	30.21	AAAA N
ATOM	850	CA	ALA	86	34.257	15.325	60.670	1.00	34.10	AAAA C
ATOM	851	CB	ALA	86	33.999	15.370	62.157	1.00	25.48	AAAA C
ATOM	852	C	ALA	86	34.729	13.962	60.216	1.00	32.67	AAAA C
ATOM	853	O	ALA	86	35.795	13.481	60.577	1.00	35.10	AAAA O
ATOM	854	N	LEU	87	33.832	13.173	59.597	1.00	28.56	AAAA N
ATOM	856	CA	LEU	87	34.188	11.805	59.323	1.00	29.26	AAAA C
ATOM	857	CB	LEU	87	33.798	10.860	60.471	1.00	13.64	AAAA C
ATOM	858	CG	LEU	87	33.801	9.363	60.188	1.00	25.77	AAAA C
ATOM	859	CD1	LEU	87	35.140	8.915	59.571	1.00	27.21	AAAA C
ATOM	860	CD2	LEU	87	33.637	8.432	61.393	1.00	23.52	AAAA C
ATOM	861	C	LEU	87	33.530	11.429	58.021	1.00	35.60	AAAA C
ATOM	862	O	LEU	87	32.320	11.421	58.001	1.00	38.97	AAAA O
ATOM	863	N	VAL	88	34.174	11.300	56.875	1.00	37.86	AAAA N
ATOM	865	CA	VAL	88	33.438	11.032	55.628	1.00	33.32	AAAA C
ATOM	866	CB	VAL	88	33.666	12.085	54.553	1.00	22.38	AAAA C
ATOM	867	CG1	VAL	88	32.974	11.675	53.261	1.00	19.24	AAAA C
ATOM	868	CG2	VAL	88	33.165	13.402	55.042	1.00	13.27	AAAA C
ATOM	869	C	VAL	88	33.898	9.684	55.114	1.00	31.79	AAAA C
ATOM	870	O	VAL	88	35.069	9.407	55.117	1.00	33.57	AAAA O
ATOM	871	N	ILE	89	33.078	8.728	54.822	1.00	31.08	AAAA N
ATOM	873	CA	ILE	89	33.361	7.433	54.280	1.00	30.45	AAAA C
ATOM	874	CB	ILE	89	32.941	6.384	55.296	1.00	30.17	AAAA C
ATOM	875	CG2	ILE	89	32.898	4.954	54.821	1.00	37.24	AAAA C
ATOM	876	CG1	ILE	89	33.893	6.420	56.500	1.00	24.92	AAAA C
ATOM	877	CD1	ILE	89	33.424	5.613	57.675	1.00	23.96	AAAA C
ATOM	878	C	ILE	89	32.509	7.206	53.027	1.00	40.64	AAAA C
ATOM	879	O	ILE	89	31.330	6.881	53.205	1.00	38.69	AAAA O
ATOM	880	N	PHE	90	33.082	7.464	51.845	1.00	41.45	AAAA N
ATOM	882	CA	PHE	90	32.346	7.371	50.591	1.00	37.67	AAAA C
ATOM	883	CB	PHE	90	32.347	8.776	50.110	1.00	32.17	AAAA C
ATOM	884	CG	PHE	90	31.581	9.081	48.865	1.00	39.77	AAAA C
ATOM	885	CD1	PHE	90	30.387	9.772	49.025	1.00	32.02	AAAA C
ATOM	886	CD2	PHE	90	32.052	8.721	47.620	1.00	29.28	AAAA C
ATOM	887	CE1	PHE	90	29.611	10.111	47.938	1.00	33.30	AAAA C
ATOM	888	CE2	PHE	90	31.290	9.086	46.534	1.00	43.09	AAAA C
ATOM	889	CZ	PHE	90	30.083	9.764	46.687	1.00	50.24	AAAA C
ATOM	890	C	PHE	90	32.856	6.384	49.557	1.00	40.72	AAAA C
ATOM	891	O	PHE	90	34.027	6.296	49.203	1.00	46.15	AAAA O
ATOM	892	N	GLU	91	32.024	5.519	49.001	1.00	39.16	AAAA N
ATOM	894	CA	GLU	91	32.248	4.601	47.954	1.00	42.45	AAAA C
ATOM	895	CB	GLU	91	32.479	5.231	46.583	1.00	38.08	AAAA C
ATOM	896	CG	GLU	91	31.136	5.865	46.250	1.00	58.86	AAAA C
ATOM	897	CD	GLU	91	30.855	5.776	44.757	1.00	63.55	AAAA C
ATOM	898	OE1	GLU	91	31.473	6.651	44.082	1.00	64.10	AAAA O
ATOM	899	OE2	GLU	91	30.058	4.813	44.573	1.00	63.64	AAAA O
ATOM	900	C	GLU	91	33.422	3.734	48.313	1.00	42.06	AAAA C
ATOM	901	O	GLU	91	34.298	3.411	47.587	1.00	44.71	AAAA O
ATOM	902	N	MET	92	33.352	3.209	49.482	1.00	46.52	AAAA N
ATOM	904	CA	MET	92	34.409	2.401	50.088	1.00	42.26	AAAA C
ATOM	905	CB	MET	92	34.299	2.659	51.584	1.00	38.37	AAAA C
ATOM	906	CG	MET	92	35.412	2.156	52.420	1.00	59.29	AAAA C
ATOM	907	SD	MET	92	36.802	3.306	52.401	1.00	57.67	AAAA S
ATOM	908	CE	MET	92	36.340	4.405	51.108	1.00	38.36	AAAA C
ATOM	909	C	MET	92	34.012	1.005	49.745	1.00	43.37	AAAA C
ATOM	910	O	MET	92	33.335	0.298	50.523	1.00	45.58	AAAA O
ATOM	911	N	THR	93	34.449	0.518	48.602	1.00	47.09	AAAA N
ATOM	913	CA	THR	93	34.175	-0.900	48.273	1.00	47.32	AAAA C
ATOM	914	CB	THR	93	34.666	-1.281	46.868	1.00	55.28	AAAA C
ATOM	915	OG1	THR	93	34.013	-0.488	45.892	1.00	57.81	AAAA O
ATOM	917	CG2	THR	93	34.332	-2.715	46.516	1.00	44.72	AAAA C

ATOM	918	C	THR	93	34.885	-1.874	49.196	1.00	51.83	AAAA C
ATOM	919	O	THR	93	36.115	-1.777	49.361	1.00	57.91	AAAA O
ATOM	920	N	ASN	94	34.237	-2.983	49.493	1.00	49.85	AAAA N
ATOM	922	CA	ASN	94	34.747	-4.069	50.285	1.00	45.64	AAAA C
ATOM	923	CB	ASN	94	36.241	-4.315	50.001	1.00	59.01	AAAA C
ATOM	924	CG	ASN	94	36.494	-4.849	48.599	1.00	75.44	AAAA C
ATOM	925	OD1	ASN	94	36.847	-4.081	47.688	1.00	77.49	AAAA O
ATOM	926	ND2	ASN	94	36.308	-6.153	48.408	1.00	79.63	AAAA N
ATOM	929	C	ASN	94	34.522	-3.838	51.763	1.00	42.58	AAAA C
ATOM	930	O	ASN	94	34.752	-4.814	52.501	1.00	46.36	AAAA O
ATOM	931	N	LEU	95	34.308	-2.609	52.182	1.00	37.28	AAAA N
ATOM	933	CA	LEU	95	34.324	-2.277	53.621	1.00	39.96	AAAA C
ATOM	934	CB	LEU	95	34.185	-0.786	53.851	1.00	34.05	AAAA C
ATOM	935	CG	LEU	95	34.323	-0.296	55.269	1.00	35.81	AAAA C
ATOM	936	CD1	LEU	95	35.785	-0.537	55.598	1.00	35.48	AAAA C
ATOM	937	CD2	LEU	95	33.847	1.177	55.344	1.00	25.46	AAAA C
ATOM	938	C	LEU	95	33.163	-2.986	54.275	1.00	43.75	AAAA C
ATOM	939	O	LEU	95	32.048	-2.936	53.772	1.00	44.04	AAAA O
ATOM	940	N	LYS	96	33.451	-3.863	55.213	1.00	46.50	AAAA N
ATOM	942	CA	LYS	96	32.364	-4.648	55.779	1.00	42.76	AAAA C
ATOM	943	CB	LYS	96	32.801	-6.075	55.995	1.00	41.41	AAAA C
ATOM	944	CG	LYS	96	32.760	-6.976	54.788	1.00	49.78	AAAA C
ATOM	945	CD	LYS	96	32.984	-8.446	55.127	1.00	58.09	AAAA C
ATOM	946	CE	LYS	96	33.772	-9.160	54.027	1.00	73.43	AAAA C
ATOM	947	NZ	LYS	96	34.098	-10.556	54.489	1.00	79.13	AAAA N
ATOM	951	C	LYS	96	31.970	-4.055	57.122	1.00	45.29	AAAA C
ATOM	952	O	LYS	96	30.978	-4.502	57.691	1.00	46.23	AAAA O
ATOM	953	N	ASP	97	32.685	-3.071	57.645	1.00	45.15	AAAA N
ATOM	955	CA	ASP	97	32.299	-2.384	58.861	1.00	42.15	AAAA C
ATOM	956	CB	ASP	97	32.294	-3.292	60.059	1.00	45.39	AAAA C
ATOM	957	CG	ASP	97	33.662	-3.562	60.624	1.00	56.95	AAAA C
ATOM	958	OD1	ASP	97	34.579	-2.825	61.012	1.00	59.88	AAAA O
ATOM	959	OD2	ASP	97	33.931	-4.782	60.714	1.00	56.01	AAAA O
ATOM	960	C	ASP	97	33.209	-1.224	59.201	1.00	41.25	AAAA C
ATOM	961	O	ASP	97	34.160	-1.074	58.437	1.00	47.03	AAAA O
ATOM	962	N	ILE	98	32.822	-0.366	60.129	1.00	40.41	AAAA N
ATOM	964	CA	ILE	98	33.675	0.820	60.340	1.00	37.83	AAAA C
ATOM	965	CB	ILE	98	32.983	2.006	61.006	1.00	38.99	AAAA C
ATOM	966	CG2	ILE	98	34.007	3.133	61.207	1.00	38.95	AAAA C
ATOM	967	CG1	ILE	98	31.835	2.488	60.092	1.00	34.84	AAAA C
ATOM	968	CD1	ILE	98	31.629	3.958	59.948	1.00	39.29	AAAA C
ATOM	969	C	ILE	98	34.854	0.322	61.114	1.00	35.11	AAAA C
ATOM	970	O	ILE	98	35.970	0.669	60.841	1.00	43.05	AAAA O
ATOM	971	N	GLY	99	34.618	-0.393	62.192	1.00	34.22	AAAA N
ATOM	973	CA	GLY	99	35.477	-0.972	63.121	1.00	33.74	AAAA C
ATOM	974	C	GLY	99	36.279	-0.084	64.024	1.00	35.90	AAAA C
ATOM	975	O	GLY	99	37.023	-0.572	64.899	1.00	38.21	AAAA O
ATOM	976	N	LEU	100	36.190	1.221	63.913	1.00	33.35	AAAA N
ATOM	978	CA	LEU	100	36.763	2.215	64.771	1.00	31.65	AAAA C
ATOM	979	CB	LEU	100	36.496	3.636	64.294	1.00	29.87	AAAA C
ATOM	980	CG	LEU	100	36.943	3.980	62.835	1.00	32.13	AAAA C
ATOM	981	CD1	LEU	100	36.710	5.479	62.610	1.00	21.38	AAAA C
ATOM	982	CD2	LEU	100	38.412	3.599	62.644	1.00	37.68	AAAA C
ATOM	983	C	LEU	100	36.312	1.976	66.194	1.00	31.94	AAAA C
ATOM	984	O	LEU	100	35.950	2.863	66.979	1.00	31.95	AAAA O
ATOM	985	N	TYR	101	36.704	0.851	66.779	1.00	31.87	AAAA N
ATOM	987	CA	TYR	101	36.329	0.395	68.071	1.00	33.33	AAAA C
ATOM	988	CB	TYR	101	36.491	-1.104	68.264	1.00	41.03	AAAA C
ATOM	989	CG	TYR	101	37.919	-1.559	68.369	1.00	46.66	AAAA C
ATOM	990	CD1	TYR	101	38.571	-1.380	69.587	1.00	51.20	AAAA C
ATOM	991	CE1	TYR	101	39.901	-1.743	69.749	1.00	49.44	AAAA C
ATOM	992	CD2	TYR	101	38.615	-2.112	67.322	1.00	45.15	AAAA C
ATOM	993	CE2	TYR	101	39.927	-2.505	67.479	1.00	47.08	AAAA C
ATOM	994	CZ	TYR	101	40.548	-2.321	68.688	1.00	49.43	AAAA C
ATOM	995	OH	TYR	101	41.834	-2.662	68.997	1.00	55.82	AAAA O
ATOM	997	C	TYR	101	36.989	1.059	69.214	1.00	33.46	AAAA C
ATOM	998	O	TYR	101	36.630	0.813	70.375	1.00	43.00	AAAA O
ATOM	999	N	ASN	102	37.752	2.091	69.068	1.00	38.12	AAAA N
ATOM	1001	CA	ASN	102	38.093	2.979	70.223	1.00	30.79	AAAA C
ATOM	1002	CB	ASN	102	39.603	2.911	70.363	1.00	48.63	AAAA C
ATOM	1003	CG	ASN	102	40.112	1.804	71.268	1.00	54.01	AAAA C
ATOM	1004	OD1	ASN	102	39.735	1.864	72.454	1.00	47.22	AAAA O
ATOM	1005	ND2	ASN	102	40.864	0.845	70.767	1.00	43.08	AAAA N
ATOM	1008	C	ASN	102	37.673	4.385	69.947	1.00	33.82	AAAA C
ATOM	1009	O	ASN	102	38.047	5.364	70.592	1.00	39.84	AAAA O
ATOM	1010	N	LEU	103	36.845	4.640	68.882	1.00	35.28	AAAA N
ATOM	1012	CA	LEU	103	36.473	6.040	68.621	1.00	36.57	AAAA C
ATOM	1013	CB	LEU	103	35.948	6.140	67.213	1.00	34.77	AAAA C
ATOM	1014	CG	LEU	103	35.525	7.482	66.612	1.00	30.32	AAAA C
ATOM	1015	CD1	LEU	103	36.606	8.513	66.646	1.00	23.20	AAAA C
ATOM	1016	CD2	LEU	103	35.199	7.169	65.146	1.00	37.10	AAAA C
ATOM	1017	C	LEU	103	35.484	6.508	69.691	1.00	37.31	AAAA C
ATOM	1018	O	LEU	103	34.449	5.874	69.837	1.00	34.26	AAAA O
ATOM	1019	N	ARG	104	35.810	7.456	70.563	1.00	33.31	AAAA N
ATOM	1021	CA	ARG	104	34.920	7.841	71.605	1.00	29.66	AAAA C

ATOM	1022	CB	ARG	104	35.568	7.657	73.018	1.00	38.17	AAAA C
ATOM	1023	CG	ARG	104	36.356	6.375	73.165	1.00	48.37	AAAA C
ATOM	1024	CD	ARG	104	35.425	5.183	73.248	1.00	50.71	AAAA C
ATOM	1025	NE	ARG	104	34.582	5.320	74.413	1.00	52.38	AAAA N
ATOM	1027	CZ	ARG	104	34.900	4.847	75.621	1.00	72.73	AAAA C
ATOM	1028	NH1	ARG	104	36.047	4.214	75.800	1.00	81.87	AAAA N
ATOM	1031	NH2	ARG	104	33.990	5.070	76.577	1.00	78.27	AAAA N
ATOM	1034	C	ARG	104	34.466	9.273	71.540	1.00	32.58	AAAA C
ATOM	1035	O	ARG	104	33.553	9.743	72.223	1.00	39.89	AAAA O
ATOM	1036	N	ASN	105	34.992	10.065	70.637	1.00	33.47	AAAA N
ATOM	1038	CA	ASN	105	34.549	11.450	70.590	1.00	30.97	AAAA C
ATOM	1044	C	ASN	105	34.907	12.149	69.310	1.00	31.00	AAAA C
ATOM	1045	O	ASN	105	36.086	12.067	69.050	1.00	37.79	AAAA O
ATOM	1039	CB	ASN	105	35.203	12.199	71.721	1.00	12.28	AAAA C
ATOM	1040	CG	ASN	105	34.786	13.568	71.756	1.00	24.93	AAAA C
ATOM	1041	OD1	ASN	105	35.125	14.549	71.127	1.00	38.14	AAAA O
ATOM	1042	ND2	ASN	105	33.828	13.985	72.649	1.00	35.96	AAAA N
ATOM	1046	N	ILE	106	33.969	12.669	68.576	1.00	31.90	AAAA N
ATOM	1048	CA	ILE	106	34.129	13.551	67.469	1.00	23.39	AAAA C
ATOM	1049	CB	ILE	106	33.239	13.185	66.307	1.00	16.54	AAAA C
ATOM	1050	CG2	ILE	106	33.132	14.408	65.374	1.00	20.38	AAAA C
ATOM	1051	CG1	ILE	106	33.928	12.034	65.558	1.00	18.30	AAAA C
ATOM	1052	CD1	ILE	106	33.055	11.293	64.643	1.00	25.48	AAAA C
ATOM	1053	C	ILE	106	33.803	14.909	68.009	1.00	27.40	AAAA C
ATOM	1054	O	ILE	106	32.628	15.106	68.243	1.00	32.86	AAAA O
ATOM	1055	N	THR	107	34.719	15.789	68.350	1.00	30.43	AAAA N
ATOM	1057	CA	THR	107	34.532	16.983	69.145	1.00	28.27	AAAA C
ATOM	1058	CB	THR	107	35.902	17.607	69.579	1.00	35.78	AAAA C
ATOM	1059	OG1	THR	107	36.819	16.503	69.738	1.00	40.26	AAAA O
ATOM	1061	CG2	THR	107	35.954	18.411	70.855	1.00	28.13	AAAA C
ATOM	1062	C	THR	107	33.728	17.950	69.332	1.00	27.95	AAAA C
ATOM	1063	O	THR	107	33.392	19.060	68.831	1.00	32.99	AAAA O
ATOM	1064	N	ARG	108	33.669	17.777	67.019	1.00	30.28	AAAA N
ATOM	1066	CA	ARG	108	33.046	18.809	66.180	1.00	31.25	AAAA C
ATOM	1067	CB	ARG	108	33.965	20.011	65.951	1.00	25.13	AAAA C
ATOM	1068	CG	ARG	108	33.105	21.174	65.543	1.00	30.68	AAAA C
ATOM	1069	CD	ARG	108	33.917	22.444	65.529	1.00	17.12	AAAA C
ATOM	1070	NE	ARG	108	33.511	23.376	64.451	1.00	33.40	AAAA N
ATOM	1072	CZ	ARG	108	34.045	23.608	63.266	1.00	46.41	AAAA C
ATOM	1073	NH1	ARG	108	35.162	22.929	62.868	1.00	40.30	AAAA N
ATOM	1076	NH2	ARG	108	33.454	24.543	62.494	1.00	39.82	AAAA N
ATOM	1079	C	ARG	108	32.701	18.328	64.784	1.00	31.50	AAAA C
ATOM	1080	O	ARG	108	33.379	17.381	64.430	1.00	32.67	AAAA O
ATOM	1081	N	GLY	109	31.567	18.809	64.284	1.00	32.60	AAAA N
ATOM	1083	CA	GLY	109	31.082	18.385	62.983	1.00	28.87	AAAA C
ATOM	1084	C	GLY	109	30.470	17.008	63.001	1.00	32.32	AAAA C
ATOM	1085	O	GLY	109	30.471	16.306	64.006	1.00	38.03	AAAA O
ATOM	1086	N	ALA	110	29.920	16.560	61.894	1.00	34.11	AAAA N
ATOM	1088	CA	ALA	110	29.086	15.371	61.833	1.00	36.77	AAAA C
ATOM	1089	CB	ALA	110	27.708	15.721	61.223	1.00	15.32	AAAA C
ATOM	1090	C	ALA	110	29.745	14.335	60.957	1.00	32.12	AAAA C
ATOM	1091	O	ALA	110	30.921	14.332	60.687	1.00	34.11	AAAA O
ATOM	1092	N	ILE	111	29.030	13.337	60.557	1.00	26.55	AAAA N
ATOM	1094	CA	ILE	111	29.569	12.273	59.771	1.00	32.90	AAAA C
ATOM	1095	CB	ILE	111	29.669	10.967	60.591	1.00	38.07	AAAA C
ATOM	1096	CG2	ILE	111	30.091	11.140	62.036	1.00	34.05	AAAA C
ATOM	1097	CG1	ILE	111	28.345	10.237	60.684	1.00	26.54	AAAA C
ATOM	1098	CD1	ILE	111	28.437	8.872	61.407	1.00	27.11	AAAA C
ATOM	1099	C	ILE	111	28.738	11.928	58.521	1.00	33.98	AAAA C
ATOM	1100	O	ILE	111	27.533	12.179	58.532	1.00	32.15	AAAA O
ATOM	1101	N	ARG	112	29.432	11.423	57.501	1.00	30.54	AAAA N
ATOM	1103	CA	ARG	112	28.773	11.107	56.247	1.00	27.48	AAAA C
ATOM	1104	CB	ARG	112	29.186	12.085	55.169	1.00	26.35	AAAA C
ATOM	1105	CG	ARG	112	28.548	11.653	53.816	1.00	25.83	AAAA C
ATOM	1106	CD	ARG	112	28.659	12.912	52.992	1.00	32.92	AAAA C
ATOM	1107	NE	ARG	112	27.950	12.726	51.770	1.00	50.34	AAAA N
ATOM	1109	CZ	ARG	112	27.778	13.503	50.720	1.00	47.61	AAAA C
ATOM	1110	NH1	ARG	112	28.334	14.695	50.696	1.00	44.92	AAAA N
ATOM	1113	NH2	ARG	112	27.012	12.925	49.789	1.00	46.00	AAAA N
ATOM	1116	C	ARG	112	29.200	9.738	55.791	1.00	29.74	AAAA C
ATOM	1117	O	ARG	112	30.343	9.611	55.406	1.00	36.52	AAAA O
ATOM	1118	N	ILE	113	28.326	8.754	55.886	1.00	33.99	AAAA N
ATOM	1120	CA	ILE	113	28.612	7.376	55.555	1.00	36.26	AAAA C
ATOM	1121	CB	ILE	113	28.457	6.461	56.760	1.00	33.27	AAAA C
ATOM	1122	CG2	ILE	113	28.850	5.021	56.449	1.00	15.85	AAAA C
ATOM	1123	CG1	ILE	113	29.374	7.012	57.874	1.00	31.92	AAAA C
ATOM	1124	CD1	ILE	113	29.324	6.250	59.176	1.00	42.34	AAAA C
ATOM	1125	C	ILE	113	27.729	6.959	54.398	1.00	39.26	AAAA C
ATOM	1126	O	ILE	113	26.637	6.482	54.664	1.00	50.72	AAAA O
ATOM	1127	N	GLU	114	28.175	7.199	53.190	1.00	35.86	AAAA N
ATOM	1129	CA	GLU	114	27.491	7.103	51.935	1.00	38.76	AAAA C
ATOM	1130	CB	GLU	114	27.471	8.443	51.216	1.00	25.58	AAAA C
ATOM	1131	CG	GLU	114	26.567	8.402	49.969	1.00	27.97	AAAA C
ATOM	1132	CD	GLU	114	26.349	9.840	49.578	1.00	36.85	AAAA C
ATOM	1133	OE1	GLU	114	26.763	10.662	50.414	1.00	45.57	AAAA O

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ATOM   1134  OE2 GLU   114      25.787  10.106  48.488  1.00 35.53      AAAA O
ATOM   1135  C   GLU   114      28.039   6.672  50.944  1.00 44.17      AAAA C
ATOM   1136  O   GLU   114      29.120   5.538  51.090  1.00 49.97      AAAA O
ATOM   1137  N   LYS   115      27.191   5.556  50.096  1.00 40.55      AAAA N
ATOM   1139  CA  LYS   115      27.219   4.440  49.242  1.00 41.16      AAAA C
ATOM   1140  CB  LYS   115      27.275   4.764  47.718  1.00 23.62      AAAA C
ATOM   1141  CG  LYS   115      27.019   6.194  47.411  1.00 18.39      AAAA C
ATOM   1142  CD  LYS   115      26.537   6.355  45.982  1.00 24.74      AAAA C
ATOM   1143  CE  LYS   115      26.751   7.804  45.622  1.00 41.86      AAAA C
ATOM   1144  NZ  LYS   115      27.165   8.045  44.196  1.00 60.91      AAAA N
ATOM   1148  C   LYS   115      28.287   3.421  49.611  1.00 42.39      AAAA C
ATOM   1149  O   LYS   115      29.102   3.103  48.749  1.00 46.68      AAAA O
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ATOM   1153  CB  ASN   116      29.534   1.868  52.381  1.00 46.12      AAAA C
ATOM   1154  CG  ASN   116      30.372   3.153  52.345  1.00 48.92      AAAA C
ATOM   1155  OD1 ASN   116      31.337   3.016  51.583  1.00 38.59      AAAA O
ATOM   1156  ND2 ASN   116      29.927   4.174  53.056  1.00 37.35      AAAA N
ATOM   1159  C   ASN   116      28.275   0.277  50.974  1.00 42.52      AAAA C
ATOM   1160  O   ASN   116      28.067  -0.361  52.033  1.00 48.24      AAAA O
ATOM   1161  N   ALA   117      27.989  -0.188  49.772  1.00 40.94      AAAA N
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ATOM   1170  CB  ASP   118      29.659  -4.945  51.477  1.00 55.39      AAAA C
ATOM   1171  CG  ASP   118      29.684  -5.119  49.958  1.00 59.40      AAAA C
ATOM   1172  OD1 ASP   118      28.870  -5.976  49.608  1.00 64.40      AAAA O
ATOM   1173  OD2 ASP   118      30.448  -4.447  49.207  1.00 66.73      AAAA O
ATOM   1174  C   ASP   118      28.818  -3.586  53.353  1.00 37.29      AAAA C
ATOM   1175  O   ASP   118      29.127  -4.536  54.026  1.00 42.89      AAAA O
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ATOM   1179  CB  LEU   119      29.159  -0.389  55.145  1.00 34.31      AAAA C
ATOM   1180  CG  LEU   119      29.640   0.331  56.378  1.00 36.58      AAAA C
ATOM   1181  CD1 LEU   119      30.950  -0.101  56.948  1.00 35.77      AAAA C
ATOM   1182  CD2 LEU   119      29.791   1.830  56.104  1.00 29.68      AAAA C
ATOM   1183  C   LEU   119      27.937  -2.376  56.007  1.00 43.67      AAAA C
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ATOM   1191  SG  CYS   120      26.568  -5.622  56.639  1.00 58.32      AAAA S
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ATOM   1195  CB  TYR   121      29.189  -3.572  62.130  1.00 34.61      AAAA C
ATOM   1196  CG  TYR   121      28.950  -5.032  62.519  1.00 36.52      AAAA C
ATOM   1197  CD1 TYR   121      29.087  -6.045  61.582  1.00 33.58      AAAA C
ATOM   1198  CE1 TYR   121      28.852  -7.350  61.980  1.00 41.21      AAAA C
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ATOM   1200  CE2 TYR   121      28.297  -6.630  64.201  1.00 39.48      AAAA C
ATOM   1201  CZ  TYR   121      28.432  -7.641  63.270  1.00 46.07      AAAA C
ATOM   1202  OH  TYR   121      28.161  -8.924  63.730  1.00 49.20      AAAA O
ATOM   1204  C   TYR   121      27.674  -1.523  61.789  1.00 38.83      AAAA C
ATOM   1205  O   TYR   121      28.445  -0.778  62.369  1.00 43.22      AAAA O
ATOM   1206  N   LEU   122      26.587  -1.045  61.180  1.00 39.58      AAAA N
ATOM   1208  CA  LEU   122      26.361   0.405  61.090  1.00 44.82      AAAA C
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ATOM   1210  CG  LEU   122      26.497   2.014  59.108  1.00 44.44      AAAA C
ATOM   1211  CD1 LEU   122      25.778   2.448  57.859  1.00 32.19      AAAA C
ATOM   1212  CD2 LEU   122      26.136   3.057  60.170  1.00 47.76      AAAA C
ATOM   1213  C   LEU   122      25.212   0.910  61.935  1.00 44.85      AAAA C
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ATOM   1215  N   SER   123      24.104   0.137  61.843  1.00 40.12      AAAA N
ATOM   1217  CA  SER   123      22.949   0.435  62.703  1.00 33.98      AAAA C
ATOM   1218  CB  SER   123      21.754  -0.330  62.239  1.00 19.26      AAAA C
ATOM   1219  OG  SER   123      21.964  -1.762  62.402  1.00 34.35      AAAA O
ATOM   1221  C   SER   123      23.165   0.060  64.159  1.00 37.43      AAAA C
ATOM   1222  O   SER   123      22.326   0.280  65.025  1.00 35.33      AAAA O
ATOM   1223  N   THR   124      24.242  -0.698  64.432  1.00 39.03      AAAA N
ATOM   1225  CA  THR   124      24.554  -1.165  65.753  1.00 37.78      AAAA C
ATOM   1226  CB  THR   124      25.368  -2.461  65.719  1.00 42.39      AAAA C
ATOM   1227  OG1 THR   124      26.502  -2.020  64.924  1.00 47.70      AAAA O
ATOM   1229  CG2 THR   124      24.677  -3.622  65.006  1.00 40.93      AAAA C
ATOM   1230  C   THR   124      25.522  -0.206  66.445  1.00 39.29      AAAA C
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ATOM   1232  N   VAL   125      25.737   1.001  65.985  1.00 37.80      AAAA N
ATOM   1234  CA  VAL   125      26.594   1.964  66.661  1.00 41.06      AAAA C
ATOM   1235  CB  VAL   125      27.683   2.542  65.714  1.00 39.50      AAAA C
ATOM   1236  CG1 VAL   125      28.570   3.599  66.352  1.00 28.36      AAAA C
ATOM   1237  CG2 VAL   125      28.693   1.565  65.110  1.00 33.07      AAAA C
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ATOM	1238	C	VAL	125	25.759	3.127	67.179	1.00 41.17	AAAA C
ATOM	1239	O	VAL	125	24.941	3.750	66.531	1.00 41.22	AAAA O
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ATOM	1242	CA	ASP	126	25.310	4.734	68.967	1.00 37.44	AAAA C
ATOM	1243	CB	ASP	126	24.862	4.335	70.342	1.00 34.73	AAAA C
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ATOM	1269	OG	SER	128	23.433	8.917	71.424	1.00 28.96	AAAA O
ATOM	1271	C	SER	128	26.133	9.975	71.292	1.00 32.39	AAAA C
ATOM	1272	O	SER	128	26.212	10.957	72.134	1.00 30.91	AAAA O
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ATOM	1284	CA	ILE	130	30.480	9.743	70.144	1.00 41.35	AAAA C
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ATOM	1289	C	ILE	130	30.305	11.178	69.679	1.00 46.48	AAAA C
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ATOM	1295	CG	LEU	131	28.823	13.805	65.878	1.00 36.79	AAAA C
ATOM	1296	CD1	LEU	131	29.128	11.405	65.324	1.00 30.15	AAAA C
ATOM	1297	CD2	LEU	131	27.625	13.581	65.334	1.00 19.92	AAAA C
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ATOM	1299	O	LEU	131	26.599	12.867	69.311	1.00 37.75	AAAA O
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ATOM	1304	CG	ASP	132	27.349	17.137	71.834	1.00 43.29	AAAA C
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ATOM	1306	OD2	ASP	132	27.413	18.331	72.208	1.00 60.58	AAAA O
ATOM	1307	C	ASP	132	25.520	15.659	68.946	1.00 43.46	AAAA C
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ATOM	1312	CB	ALA	133	25.628	17.987	66.092	1.00 33.82	AAAA C
ATOM	1313	C	ALA	133	24.694	15.669	65.775	1.00 33.33	AAAA C
ATOM	1314	O	ALA	133	24.777	15.791	64.517	1.00 33.71	AAAA O
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ATOM	1337	HD2	ASN	136	24.379	19.441	62.585	1.00	47.85	AAAA H
ATOM	1340	C	ASN	136	24.031	15.230	60.259	1.00	35.31	AAAA C
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ATOM	1380	CG1	VAL	140	22.800	8.375	50.881	1.00	25.88	AAAA C
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ATOM	1382	C	VAL	140	23.422	5.670	51.874	1.00	41.96	AAAA C
ATOM	1383	O	VAL	140	24.537	6.172	51.637	1.00	44.03	AAAA O
ATOM	1384	N	GLY	141	22.899	4.562	51.402	1.00	42.66	AAAA N
ATOM	1386	CA	GLY	141	23.381	3.805	50.278	1.00	30.94	AAAA C
ATOM	1387	C	GLY	141	24.265	2.696	50.835	1.00	38.98	AAAA C
ATOM	1388	O	GLY	141	25.132	2.003	50.176	1.00	35.87	AAAA O
ATOM	1389	N	ASN	142	23.985	2.418	52.116	1.00	38.92	AAAA N
ATOM	1391	CA	ASN	142	24.858	1.390	52.746	1.00	44.32	AAAA C
ATOM	1392	CB	ASN	142	25.257	1.774	54.187	1.00	43.12	AAAA C
ATOM	1393	CG	ASN	142	26.131	3.022	54.152	1.00	42.00	AAAA C
ATOM	1394	OD1	ASN	142	26.984	3.077	53.269	1.00	40.47	AAAA O
ATOM	1395	ND2	ASN	142	25.945	4.022	55.019	1.00	41.98	AAAA N
ATOM	1398	C	ASN	142	24.153	0.066	52.687	1.00	45.84	AAAA C
ATOM	1399	O	ASN	142	23.113	-0.015	52.055	1.00	49.65	AAAA O
ATOM	1400	N	LYS	143	24.674	-0.990	53.272	1.00	45.23	AAAA N
ATOM	1402	CA	LYS	143	24.073	-2.299	53.195	1.00	49.14	AAAA C
ATOM	1403	CB	LYS	143	25.166	-3.328	53.433	1.00	41.49	AAAA C
ATOM	1404	CG	LYS	143	24.750	-4.686	53.832	1.00	44.96	AAAA C
ATOM	1405	CD	LYS	143	25.512	-5.743	53.100	1.00	48.66	AAAA C
ATOM	1406	CE	LYS	143	25.043	-7.131	53.558	1.00	38.35	AAAA C
ATOM	1407	NZ	LYS	143	26.080	-8.093	53.040	1.00	53.83	AAAA N
ATOM	1411	C	LYS	143	22.902	-2.431	54.169	1.00	52.85	AAAA C
ATOM	1412	O	LYS	143	22.960	-2.099	55.360	1.00	55.21	AAAA O
ATOM	1413	N	PRO	144	21.806	-3.047	53.731	1.00	52.39	AAAA N
ATOM	1414	CD	PRO	144	21.617	-3.469	52.315	1.00	52.58	AAAA C
ATOM	1415	CA	PRO	144	20.559	-3.118	54.489	1.00	48.30	AAAA C
ATOM	1416	CB	PRO	144	19.549	-3.602	53.455	1.00	51.41	AAAA C
ATOM	1417	CG	PRO	144	20.134	-3.299	52.099	1.00	50.41	AAAA C
ATOM	1418	C	PRO	144	20.621	-4.050	55.659	1.00	44.65	AAAA C
ATOM	1419	O	PRO	144	20.904	-5.236	55.501	1.00	36.84	AAAA O
ATOM	1420	N	PRO	145	20.318	-3.533	56.859	1.00	45.12	AAAA N
ATOM	1421	CD	PRO	145	20.123	-2.054	57.094	1.00	38.17	AAAA C
ATOM	1422	CA	PRO	145	20.448	-4.233	58.128	1.00	40.19	AAAA C
ATOM	1423	CB	PRO	145	19.704	-3.288	59.099	1.00	37.08	AAAA C
ATOM	1424	CG	PRO	145	20.040	-1.910	58.602	1.00	33.65	AAAA C
ATOM	1425	C	PRO	145	19.993	-5.655	58.155	1.00	47.17	AAAA C
ATOM	1426	O	PRO	145	20.556	-6.592	58.768	1.00	48.05	AAAA O
ATOM	1427	N	LYS	146	18.979	-5.924	57.489	1.00	53.72	AAAA N
ATOM	1429	CA	LYS	146	18.268	-7.229	57.295	1.00	56.94	AAAA C
ATOM	1430	CB	LYS	146	16.894	-7.050	56.647	1.00	65.44	AAAA C
ATOM	1431	CG	LYS	146	16.220	-8.232	55.982	1.00	64.32	AAAA C
ATOM	1432	CD	LYS	146	14.797	-8.422	56.451	0.01	62.75	AAAA C
ATOM	1433	CE	LYS	146	14.194	-9.717	55.934	0.01	62.14	AAAA C
ATOM	1434	NZ	LYS	146	12.720	-9.610	55.753	0.01	61.38	AAAA N
ATOM	1436	C	LYS	146	19.138	-8.138	56.446	1.00	61.40	AAAA C
ATOM	1439	O	LYS	146	19.237	-9.346	56.732	1.00	66.22	AAAA O
ATOM	1440	N	GLU	147	19.779	-7.649	55.399	1.00	62.92	AAAA N
ATOM	1442	CA	GLU	147	20.923	-8.446	54.742	1.00	67.00	AAAA C
ATOM	1443	CB	GLU	147	21.101	-8.070	53.294	1.00	62.32	AAAA C

ATOM	1444	CG	GLU	147	19.867	-7.579	52.567	1.00	73.15	AAAA C
ATOM	1445	CD	GLU	147	20.164	-7.413	51.093	1.00	85.90	AAAA C
ATOM	1446	OE1	GLU	147	21.339	-7.636	50.701	1.00	95.25	AAAA O
ATOM	1447	OE2	GLU	147	19.201	-7.053	50.376	1.00	87.47	AAAA O
ATOM	1448	C	GLU	147	22.136	-8.470	55.541	1.00	69.40	AAAA C
ATOM	1449	O	GLU	147	22.883	-9.437	55.361	1.00	72.86	AAAA O
ATOM	1450	N	CYS	148	22.506	-7.484	56.355	1.00	66.76	AAAA N
ATOM	1452	CA	CYS	148	23.693	-7.588	57.183	1.00	64.65	AAAA C
ATOM	1453	C	CYS	148	23.598	-8.702	58.196	1.00	65.56	AAAA C
ATOM	1454	O	CYS	148	24.473	-9.524	58.414	1.00	65.89	AAAA O
ATOM	1455	CB	CYS	148	23.952	-6.301	58.001	1.00	57.29	AAAA C
ATOM	1456	SG	CYS	148	24.565	-5.091	56.808	1.00	59.22	AAAA S
ATOM	1457	N	GLY	149	22.514	-8.743	58.977	1.00	67.88	AAAA N
ATOM	1459	CA	GLY	149	22.387	-9.744	60.029	1.00	62.15	AAAA C
ATOM	1460	C	GLY	149	23.443	-9.627	61.120	1.00	59.18	AAAA C
ATOM	1461	O	GLY	149	23.925	-10.603	61.699	1.00	61.11	AAAA O
ATOM	1462	N	ASP	150	23.717	-8.426	61.596	1.00	54.88	AAAA N
ATOM	1464	CA	ASP	150	24.794	-8.198	62.533	1.00	55.78	AAAA C
ATOM	1465	CB	ASP	150	25.041	-6.703	62.750	1.00	49.10	AAAA C
ATOM	1466	CG	ASP	150	25.320	-6.034	61.410	1.00	58.50	AAAA C
ATOM	1467	OD1	ASP	150	25.726	-6.796	60.480	1.00	57.73	AAAA O
ATOM	1468	OD2	ASP	150	25.102	-4.819	61.363	1.00	49.69	AAAA O
ATOM	1469	C	ASP	150	24.519	-8.854	63.855	1.00	59.36	AAAA C
ATOM	1470	O	ASP	150	23.392	-8.820	64.377	1.00	67.48	AAAA O
ATOM	1471	N	LEU	151	25.532	-9.369	64.524	1.00	54.39	AAAA N
ATOM	1473	CA	LEU	151	25.314	-9.908	65.853	1.00	52.79	AAAA C
ATOM	1474	CB	LEU	151	25.208	-11.409	65.806	1.00	58.55	AAAA C
ATOM	1475	CG	LEU	151	24.063	-12.101	65.092	1.00	69.45	AAAA C
ATOM	1476	CD1	LEU	151	24.515	-13.421	64.489	1.00	65.26	AAAA C
ATOM	1477	CD2	LEU	151	22.837	-12.372	65.951	1.00	65.43	AAAA C
ATOM	1478	C	LEU	151	26.409	-9.454	66.805	1.00	51.93	AAAA C
ATOM	1479	O	LEU	151	27.598	-9.734	66.634	1.00	55.59	AAAA O
ATOM	1480	N	CYS	152	26.024	-8.773	67.849	1.00	48.62	AAAA N
ATOM	1482	CA	CYS	152	26.992	-8.189	68.740	1.00	56.73	AAAA C
ATOM	1483	C	CYS	152	27.650	-9.325	69.493	1.00	63.58	AAAA C
ATOM	1484	O	CYS	152	27.074	-10.405	69.575	1.00	62.40	AAAA O
ATOM	1485	CB	CYS	152	26.358	-7.144	69.657	1.00	41.99	AAAA C
ATOM	1486	SG	CYS	152	25.985	-5.635	68.703	1.00	55.83	AAAA S
ATOM	1487	N	PRO	153	28.826	-9.072	70.059	1.00	68.05	AAAA N
ATOM	1488	CD	PRO	153	29.618	-7.838	69.903	1.00	66.66	AAAA C
ATOM	1489	CA	PRO	153	29.497	-10.094	70.851	1.00	70.60	AAAA C
ATOM	1490	CB	PRO	153	30.601	-9.323	71.557	1.00	69.98	AAAA C
ATOM	1491	CG	PRO	153	30.861	-8.159	70.690	1.00	70.58	AAAA C
ATOM	1492	C	PRO	153	28.543	-10.734	71.850	1.00	69.64	AAAA C
ATOM	1493	O	PRO	153	27.859	-10.075	72.615	1.00	69.58	AAAA O
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ATOM	1497	C	GLY	154	26.245	-13.230	72.223	1.00	81.75	AAAA C
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ATOM	1502	CB	THR	155	24.016	-11.661	69.705	1.00	85.07	AAAA C
ATOM	1503	OG1	THR	155	24.063	-10.417	70.420	1.00	84.51	AAAA O
ATOM	1505	CG2	THR	155	22.686	-11.995	69.092	1.00	82.27	AAAA C
ATOM	1506	C	THR	155	24.060	-14.094	70.353	1.00	93.69	AAAA C
ATOM	1507	O	THR	155	23.005	-14.664	70.617	1.00	95.92	AAAA O
ATOM	1508	N	MET	156	25.003	-14.655	69.617	1.00	97.23	AAAA N
ATOM	1510	CA	MET	156	24.884	-15.973	69.024	1.00	99.05	AAAA C
ATOM	1511	CB	MET	156	25.907	-16.190	67.896	1.00	100.40	AAAA C
ATOM	1512	CG	MET	156	25.456	-15.675	66.542	0.01	99.75	AAAA C
ATOM	1513	SD	MET	156	23.687	-15.857	66.255	0.01	99.72	AAAA S
ATOM	1514	CE	MET	156	23.664	-17.214	65.087	0.01	99.59	AAAA C
ATOM	1515	C	MET	156	25.027	-17.106	70.032	1.00	100.57	AAAA C
ATOM	1516	O	MET	156	24.353	-18.122	69.835	1.00	101.64	AAAA O
ATOM	1517	N	ALA	157	25.974	-17.057	70.967	1.00	100.53	AAAA N
ATOM	1519	CA	ALA	157	26.022	-18.102	71.986	1.00	101.00	AAAA C
ATOM	1520	CB	ALA	157	27.317	-18.158	72.766	1.00	103.42	AAAA C
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ATOM	1525	CA	GLU	158	23.935	-16.629	74.781	1.00	97.43	AAAA C
ATOM	1526	CB	GLU	158	23.128	-17.865	75.208	1.00	105.93	AAAA C
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ATOM	1529	OE1	GLU	158	21.284	-15.733	74.096	1.00	126.27	AAAA O
ATOM	1530	OE2	GLU	158	21.199	-15.317	76.282	1.00	117.79	AAAA O
ATOM	1531	C	GLU	158	24.434	-15.915	76.025	1.00	95.00	AAAA C
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ATOM	1537	OG	SER	159	26.972	-14.427	78.886	1.00	98.08	AAAA O
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ATOM	1540	O	SER	159	27.368	-12.592	75.810	1.00	92.75	AAAA O
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ATOM  1542  CD  PRO  160      23.789 -12.122  76.395  1.00 86.67      AAAA C
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ATOM  1544  CB  PRO  160      24.125  -9.978  75.456  1.00 84.79      AAAA C
ATOM  1545  CG  PRO  160      23.370 -10.671  76.515  1.00 84.62      AAAA C
ATOM  1546  C   PRO  160      26.503 -10.025  76.236  1.00 79.60      AAAA C
ATOM  1547  O   PRO  160      26.319  -9.934  77.456  1.00 79.70      AAAA O
ATOM  1548  N   MET  161      27.563  -9.522  75.596  1.00 74.45      AAAA N
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ATOM  1551  CB  MET  161      29.924  -9.178  76.038  1.00 69.93      AAAA C
ATOM  1552  CG  MET  161      30.118 -10.630  75.706  1.00 71.43      AAAA C
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ATOM  1560  C   CYS  162      26.306  -4.777  75.670  1.00 51.52      AAAA C
ATOM  1561  O   CYS  162      25.224  -5.324  75.928  1.00 53.89      AAAA O
ATOM  1562  CB  CYS  162      27.422  -5.099  73.459  1.00 48.31      AAAA C
ATOM  1563  SG  CYS  162      28.533  -6.064  72.432  1.00 54.02      AAAA S
ATOM  1564  N   GLU  163      26.409  -3.522  76.031  1.00 46.31      AAAA N
ATOM  1566  CA  GLU  163      25.355  -2.675  76.538  1.00 47.19      AAAA C
ATOM  1567  CB  GLU  163      26.051  -1.412  77.027  1.00 49.95      AAAA C
ATOM  1568  CG  GLU  163      26.476  -1.364  78.465  1.00 62.30      AAAA C
ATOM  1569  CD  GLU  163      25.817  -0.135  79.116  1.00 81.67      AAAA C
ATOM  1570  OE1 GLU  163      26.470   0.473  80.016  1.00 73.22      AAAA O
ATOM  1571  OE2 GLU  163      24.646   0.208  78.721  1.00 80.93      AAAA O
ATOM  1572  C   GLU  163      24.299  -2.340  75.472  1.00 49.05      AAAA C
ATOM  1573  O   GLU  163      24.488  -2.423  74.234  1.00 45.90      AAAA O
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ATOM  1576  CA  LYS  164      22.011  -1.499  75.081  1.00 43.92      AAAA C
ATOM  1577  CB  LYS  164      20.714  -2.244  75.450  1.00 44.48      AAAA C
ATOM  1578  CG  LYS  164      20.560  -3.639  74.870  1.00 48.65      AAAA C
ATOM  1579  CD  LYS  164      19.480  -4.432  75.622  1.00 49.04      AAAA C
ATOM  1580  CE  LYS  164      18.409  -5.012  74.720  1.00 49.21      AAAA C
ATOM  1581  NZ  LYS  164      17.951  -6.372  75.134  1.00 37.67      AAAA N
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ATOM  1590  CB  THR  165      21.831   2.952  73.553  1.00 47.81      AAAA C
ATOM  1591  OG1 THR  165      22.053   2.689  72.127  1.00 39.13      AAAA O
ATOM  1593  CG2 THR  165      23.119   2.842  74.362  1.00 40.40      AAAA C
ATOM  1594  C   THR  165      19.532   1.881  73.189  1.00 40.92      AAAA C
ATOM  1595  O   THR  165      19.346   0.897  72.414  1.00 35.91      AAAA O
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ATOM  1598  CA  THR  166      17.689   2.991  72.182  1.00 42.97      AAAA C
ATOM  1599  CB  THR  166      16.297   3.096  72.833  1.00 55.99      AAAA C
ATOM  1600  OG1 THR  166      15.662   4.385  72.819  1.00 41.42      AAAA O
ATOM  1602  CG2 THR  166      16.157   2.740  74.313  1.00 42.83      AAAA C
ATOM  1603  C   THR  166      17.983   4.051  71.137  1.00 40.17      AAAA C
ATOM  1604  O   THR  166      18.219   5.206  71.509  1.00 35.72      AAAA O
ATOM  1605  N   ILE  167      17.912   3.725  69.866  1.00 42.21      AAAA N
ATOM  1607  CA  ILE  167      18.182   4.672  68.777  1.00 41.05      AAAA C
ATOM  1608  CB  ILE  167      19.437   4.335  67.904  1.00 39.50      AAAA C
ATOM  1609  CG2 ILE  167      19.589   5.346  66.716  1.00 15.26      AAAA C
ATOM  1610  CG1 ILE  167      20.722   4.305  68.724  1.00 36.20      AAAA C
ATOM  1611  CD1 ILE  167      21.899   3.665  67.966  1.00 35.70      AAAA C
ATOM  1612  C   ILE  167      16.937   4.524  67.882  1.00 40.94      AAAA C
ATOM  1613  O   ILE  167      16.655   3.435  67.394  1.00 35.51      AAAA O
ATOM  1614  N   ASN  168      16.318   5.635  67.537  1.00 42.29      AAAA N
ATOM  1616  CA  ASN  168      15.112   5.633  66.713  1.00 45.22      AAAA C
ATOM  1617  CB  ASN  168      15.526   5.253  65.292  1.00 45.69      AAAA C
ATOM  1618  CG  ASN  168      14.497   5.696  64.244  1.00 51.19      AAAA C
ATOM  1619  OD1 ASN  168      14.344   5.112  63.150  1.00 41.75      AAAA O
ATOM  1620  ND2 ASN  168      13.749   6.763  64.522  1.00 48.89      AAAA N
ATOM  1623  C   ASN  168      13.954   4.739  67.141  1.00 46.55      AAAA C
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ATOM  1627  CA  ASN  169      12.717   3.759  69.007  1.00 43.67      AAAA C
ATOM  1628  CB  ASN  169      11.315   4.106  68.540  1.00 36.84      AAAA C
ATOM  1629  CG  ASN  169      10.943   5.487  69.093  1.00 42.75      AAAA C
ATOM  1630  OD1 ASN  169      10.917   5.779  70.280  1.00 36.67      AAAA O
ATOM  1631  ND2 ASN  169      10.658   6.448  68.213  1.00 40.74      AAAA N
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ATOM  1638  CA  GLU  170      14.655   0.513  68.850  1.00 45.88      AAAA C
ATOM  1639  CB  GLU  170      15.283   0.278  67.524  1.00 55.92      AAAA C
ATOM  1640  CG  GLU  170      15.028  -0.953  66.702  1.00 67.08      AAAA C
ATOM  1641  CD  GLU  170      14.517  -0.605  65.294  1.00 74.56      AAAA C
ATOM  1642  OE1 GLU  170      13.869   0.466  65.049  1.00 77.75      AAAA O
ATOM  1643  OE2 GLU  170      14.763  -1.437  64.389  1.00 70.71      AAAA O
ATOM  1644  C   GLU  170      15.647   0.379  70.010  1.00 47.19      AAAA C
ATOM  1645  O   GLU  170      16.582   1.172  70.213  1.00 49.92      AAAA O
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ATOM	1646	N	TYR	171	15.344	-0.462	70.952	1.00	49.10	AAAA N
ATOM	1648	CA	TYR	171	16.231	-0.688	72.097	1.00	51.81	AAAA C
ATOM	1649	CB	TYR	171	15.434	-0.861	73.359	1.00	49.94	AAAA C
ATOM	1650	CG	TYR	171	16.175	-1.168	74.620	1.00	48.90	AAAA C
ATOM	1651	CD1	TYR	171	16.980	-0.210	75.237	1.00	46.46	AAAA C
ATOM	1652	CE1	TYR	171	17.634	-0.469	76.407	1.00	41.17	AAAA C
ATOM	1653	CD2	TYR	171	16.065	-2.429	75.194	1.00	43.62	AAAA C
ATOM	1654	CE2	TYR	171	16.734	-2.675	76.366	1.00	44.44	AAAA C
ATOM	1655	CZ	TYR	171	17.516	-1.718	76.973	1.00	43.58	AAAA C
ATOM	1656	OH	TYR	171	18.174	-2.017	78.146	1.00	40.16	AAAA O
ATOM	1658	C	TYR	171	17.058	-1.938	71.832	1.00	51.41	AAAA C
ATOM	1659	O	TYR	171	16.519	-3.024	71.889	1.00	52.59	AAAA O
ATOM	1660	N	ASN	172	18.331	-1.752	71.493	1.00	53.70	AAAA N
ATOM	1662	CA	ASN	172	19.203	-2.898	71.193	1.00	52.36	AAAA C
ATOM	1663	CB	ASN	172	19.085	-3.278	69.709	1.00	55.43	AAAA C
ATOM	1664	CG	ASN	172	18.939	-4.766	69.498	1.00	61.75	AAAA C
ATOM	1665	OD1	ASN	172	19.233	-5.646	70.304	1.00	61.61	AAAA O
ATOM	1666	ND2	ASN	172	18.449	-5.048	68.295	1.00	57.97	AAAA N
ATOM	1669	C	ASN	172	20.665	-2.712	71.569	1.00	43.81	AAAA C
ATOM	1670	O	ASN	172	21.163	-1.760	72.213	1.00	39.38	AAAA O
ATOM	1671	N	TYR	173	21.373	-3.796	71.393	1.00	43.20	AAAA N
ATOM	1673	CA	TYR	173	22.794	-3.929	71.698	1.00	44.76	AAAA C
ATOM	1674	CB	TYR	173	23.223	-5.374	71.514	1.00	41.66	AAAA C
ATOM	1675	CG	TYR	173	22.759	-6.274	72.630	1.00	45.18	AAAA C
ATOM	1676	CD1	TYR	173	21.931	-7.316	72.237	1.00	46.48	AAAA C
ATOM	1677	CE1	TYR	173	21.438	-8.181	73.193	1.00	51.36	AAAA C
ATOM	1678	CD2	TYR	173	23.081	-6.132	73.978	1.00	44.86	AAAA C
ATOM	1679	CE2	TYR	173	22.583	-7.016	74.916	1.00	46.92	AAAA C
ATOM	1680	CZ	TYR	173	21.757	-8.038	74.535	1.00	50.33	AAAA C
ATOM	1681	OH	TYR	173	21.171	-9.006	75.328	1.00	50.64	AAAA O
ATOM	1683	C	TYR	173	23.673	-3.099	70.762	1.00	46.94	AAAA C
ATOM	1684	O	TYR	173	23.389	-2.983	69.567	1.00	49.76	AAAA O
ATOM	1685	N	ARG	174	24.579	-2.318	71.366	1.00	47.79	AAAA N
ATOM	1687	CA	ARG	174	25.517	-1.496	70.577	1.00	49.13	AAAA C
ATOM	1688	CB	ARG	174	25.537	-0.132	71.233	1.00	44.32	AAAA C
ATOM	1689	CG	ARG	174	24.210	0.623	71.234	1.00	48.14	AAAA C
ATOM	1690	CD	ARG	174	23.372	0.344	70.003	1.00	51.47	AAAA C
ATOM	1691	NE	ARG	174	21.974	0.760	70.039	1.00	48.35	AAAA N
ATOM	1693	CZ	ARG	174	21.144	0.570	69.017	1.00	48.23	AAAA C
ATOM	1694	NH1	ARG	174	21.477	0.022	67.864	1.00	38.96	AAAA N
ATOM	1697	NH2	ARG	174	19.909	1.022	69.197	1.00	54.65	AAAA N
ATOM	1700	C	ARG	174	26.921	-2.094	70.461	1.00	45.98	AAAA C
ATOM	1701	O	ARG	174	27.548	-2.557	71.406	1.00	44.97	AAAA O
ATOM	1702	N	CYS	175	27.493	-2.183	69.294	1.00	46.21	AAAA N
ATOM	1704	CA	CYS	175	28.787	-2.758	68.997	1.00	45.60	AAAA C
ATOM	1705	C	CYS	175	29.407	-2.395	67.665	1.00	46.23	AAAA C
ATOM	1706	O	CYS	175	28.755	-2.018	66.665	1.00	44.78	AAAA O
ATOM	1707	CB	CYS	175	28.576	-4.253	69.167	1.00	35.62	AAAA C
ATOM	1708	SG	CYS	175	27.812	-5.181	67.827	1.00	51.92	AAAA S
ATOM	1709	N	TRP	176	30.764	-2.517	67.583	1.00	48.16	AAAA N
ATOM	1711	CA	TRP	176	31.430	-2.091	66.325	1.00	42.48	AAAA C
ATOM	1712	CB	TRP	176	32.769	-1.409	66.564	1.00	36.38	AAAA C
ATOM	1713	CG	TRP	176	32.689	-0.069	67.203	1.00	25.56	AAAA C
ATOM	1714	CD2	TRP	176	32.588	1.186	66.489	1.00	23.71	AAAA C
ATOM	1715	CE2	TRP	176	32.559	2.217	67.422	1.00	32.40	AAAA C
ATOM	1716	CE3	TRP	176	32.535	1.520	65.141	1.00	24.31	AAAA C
ATOM	1717	CD1	TRP	176	32.730	0.257	68.525	1.00	28.37	AAAA C
ATOM	1718	NE1	TRP	176	32.636	1.636	68.678	1.00	37.21	AAAA N
ATOM	1720	CZ2	TRP	176	32.441	3.565	67.088	1.00	28.51	AAAA C
ATOM	1721	CZ3	TRP	176	32.447	2.822	64.789	1.00	22.23	AAAA C
ATOM	1722	CH2	TRP	176	32.406	3.817	65.745	1.00	29.51	AAAA C
ATOM	1723	C	TRP	176	31.631	-3.268	65.408	1.00	39.30	AAAA C
ATOM	1724	O	TRP	176	31.703	-3.121	64.199	1.00	39.15	AAAA O
ATOM	1725	N	THR	177	31.682	-4.460	66.005	1.00	41.33	AAAA N
ATOM	1727	CA	THR	177	31.964	-5.644	65.161	1.00	49.28	AAAA C
ATOM	1728	CB	THR	177	33.480	-6.062	65.162	1.00	43.66	AAAA C
ATOM	1729	OG1	THR	177	34.309	-5.025	64.613	1.00	47.85	AAAA O
ATOM	1731	CG2	THR	177	33.676	-7.271	64.283	1.00	58.51	AAAA C
ATOM	1732	C	THR	177	31.290	-6.814	65.858	1.00	48.76	AAAA C
ATOM	1733	O	THR	177	30.982	-6.539	67.001	1.00	51.53	AAAA O
ATOM	1734	N	THR	178	31.269	-8.000	65.331	1.00	51.96	AAAA N
ATOM	1736	CA	THR	178	30.924	-9.236	65.946	1.00	58.95	AAAA C
ATOM	1737	CB	THR	178	31.253	-10.500	65.092	1.00	66.55	AAAA C
ATOM	1738	OG1	THR	178	31.505	-10.066	63.734	1.00	75.70	AAAA O
ATOM	1740	CG2	THR	178	30.104	-11.489	65.148	1.00	74.23	AAAA C
ATOM	1741	C	THR	178	31.714	-9.539	67.213	1.00	60.25	AAAA C
ATOM	1742	O	THR	178	31.204	-10.202	68.135	1.00	66.05	AAAA O
ATOM	1743	N	ASN	179	32.977	-9.130	67.253	1.00	57.56	AAAA N
ATOM	1745	CA	ASN	179	33.793	-9.392	68.443	1.00	53.39	AAAA C
ATOM	1746	CB	ASN	179	35.130	-10.024	68.068	1.00	48.46	AAAA C
ATOM	1747	CG	ASN	179	34.997	-11.218	67.126	1.00	56.25	AAAA C
ATOM	1748	OD1	ASN	179	34.412	-12.294	67.553	1.00	51.38	AAAA O
ATOM	1749	ND2	ASN	179	35.229	-11.063	65.863	1.00	48.10	AAAA N
ATOM	1752	C	ASN	179	34.096	-8.100	69.208	1.00	50.79	AAAA C
ATOM	1753	O	ASN	179	34.556	-8.377	70.428	1.00	57.97	AAAA O

ATOM	1754	N	ARG	180	33.626	-7.022	68.913	1.00 47.06	AAAA N
ATOM	1756	CA	ARG	180	33.808	-5.820	69.691	1.00 48.25	AAAA C
ATOM	1757	CB	ARG	180	34.925	-4.962	69.074	1.00 49.72	AAAA C
ATOM	1758	CG	ARG	180	36.324	-5.501	69.285	1.00 60.92	AAAA C
ATOM	1759	CD	ARG	180	37.288	-4.948	68.279	1.00 70.83	AAAA C
ATOM	1760	NE	ARG	180	38.569	-5.605	68.203	1.00 76.18	AAAA N
ATOM	1762	CZ	ARG	180	39.294	-5.895	69.276	1.00 76.59	AAAA C
ATOM	1763	NH1	ARG	180	38.877	-5.608	70.498	1.00 80.82	AAAA N
ATOM	1766	NH2	ARG	180	40.474	-6.478	69.180	1.00 79.33	AAAA N
ATOM	1769	C	ARG	180	32.530	-4.977	69.821	1.00 48.10	AAAA C
ATOM	1770	O	ARG	180	31.862	-4.476	68.905	1.00 46.99	AAAA O
ATOM	1771	N	CYS	181	32.230	-4.728	71.063	1.00 44.80	AAAA N
ATOM	1773	CA	CYS	181	31.199	-3.924	71.619	1.00 45.20	AAAA C
ATOM	1774	C	CYS	181	31.646	-2.463	71.692	1.00 44.50	AAAA C
ATOM	1775	O	CYS	181	32.835	-2.227	71.724	1.00 47.09	AAAA O
ATOM	1776	CB	CYS	181	30.940	-4.282	73.110	1.00 43.88	AAAA C
ATOM	1777	SG	CYS	181	30.363	-5.944	73.346	1.00 56.08	AAAA S
ATOM	1778	N	GLN	182	30.659	-1.600	71.690	1.00 39.30	AAAA N
ATOM	1780	CA	GLN	182	30.948	-0.177	71.690	1.00 43.43	AAAA C
ATOM	1781	CB	GLN	182	29.749	0.619	71.196	1.00 23.99	AAAA C
ATOM	1782	CG	GLN	182	29.809	2.085	71.435	1.00 28.57	AAAA C
ATOM	1783	CD	GLN	182	28.757	2.867	70.733	1.00 29.35	AAAA C
ATOM	1784	OE1	GLN	182	27.898	2.304	70.033	1.00 38.55	AAAA O
ATOM	1785	NE2	GLN	182	28.857	4.164	70.912	1.00 28.14	AAAA N
ATOM	1788	C	GLN	182	31.218	0.089	73.162	1.00 46.07	AAAA C
ATOM	1789	O	GLN	182	30.458	-0.327	74.041	1.00 47.01	AAAA O
ATOM	1790	N	LYS	183	32.213	0.866	73.524	1.00 46.98	AAAA N
ATOM	1792	CA	LYS	183	32.479	1.064	74.934	1.00 45.26	AAAA C
ATOM	1793	CB	LYS	183	33.966	1.278	75.185	1.00 48.68	AAAA C
ATOM	1794	CG	LYS	183	34.865	0.267	74.482	1.00 47.95	AAAA C
ATOM	1795	CD	LYS	183	36.337	0.734	74.523	1.00 48.06	AAAA C
ATOM	1796	CE	LYS	183	37.178	-0.208	73.684	1.00 46.78	AAAA C
ATOM	1797	NZ	LYS	183	38.499	-0.654	74.158	1.00 44.00	AAAA N
ATOM	1801	C	LYS	183	31.659	2.205	75.477	1.00 48.13	AAAA C
ATOM	1802	O	LYS	183	31.679	3.305	74.946	1.00 48.84	AAAA O
ATOM	1803	N	MET	184	31.165	2.014	76.698	1.00 52.59	AAAA N
ATOM	1805	CA	MET	184	30.388	3.041	77.413	1.00 53.22	AAAA C
ATOM	1806	CB	MET	184	28.927	2.613	77.537	1.00 54.27	AAAA C
ATOM	1807	CG	MET	184	27.855	2.955	76.536	1.00 56.16	AAAA C
ATOM	1808	SD	MET	184	26.911	1.601	75.912	1.00 57.56	AAAA S
ATOM	1809	CE	MET	184	26.738	1.855	74.171	1.00 46.57	AAAA C
ATOM	1810	C	MET	184	31.051	3.200	78.770	1.00 50.55	AAAA C
ATOM	1811	O	MET	184	31.770	2.292	79.116	1.00 48.82	AAAA O
ATOM	1812	N	CYS	185	30.796	4.195	79.565	1.00 53.97	AAAA N
ATOM	1814	CA	CYS	185	31.342	4.365	80.892	1.00 58.63	AAAA C
ATOM	1815	C	CYS	185	30.297	4.320	81.989	1.00 65.16	AAAA C
ATOM	1816	O	CYS	185	29.133	4.649	81.761	1.00 65.87	AAAA O
ATOM	1817	CB	CYS	185	31.965	5.772	81.000	1.00 60.37	AAAA C
ATOM	1818	SG	CYS	185	33.623	5.771	80.312	1.00 60.09	AAAA S
ATOM	1819	N	PRO	186	30.688	3.978	83.206	1.00 69.41	AAAA N
ATOM	1820	CD	PRO	186	32.066	3.777	83.702	1.00 71.11	AAAA C
ATOM	1821	CA	PRO	186	29.717	3.933	84.304	1.00 69.11	AAAA C
ATOM	1822	CB	PRO	186	30.523	3.487	85.503	1.00 68.03	AAAA C
ATOM	1823	CG	PRO	186	31.910	3.920	85.198	1.00 71.02	AAAA C
ATOM	1824	C	PRO	186	29.120	5.320	84.431	1.00 69.47	AAAA C
ATOM	1825	O	PRO	186	29.820	6.345	84.507	1.00 65.93	AAAA O
ATOM	1826	N	SER	187	27.801	5.367	84.546	1.00 68.78	AAAA N
ATOM	1828	CA	SER	187	27.050	6.592	84.750	1.00 69.29	AAAA C
ATOM	1829	CB	SER	187	25.594	6.287	85.129	1.00 78.29	AAAA C
ATOM	1830	OG	SER	187	25.474	4.935	85.566	1.00 91.78	AAAA O
ATOM	1832	C	SER	187	27.630	7.476	85.836	1.00 67.19	AAAA C
ATOM	1833	O	SER	187	27.606	8.708	85.803	1.00 63.98	AAAA O
ATOM	1834	N	THR	188	28.108	6.853	86.908	1.00 68.20	AAAA N
ATOM	1836	CA	THR	188	28.870	7.507	87.963	1.00 68.39	AAAA C
ATOM	1837	CB	THR	188	29.805	6.459	88.618	1.00 73.84	AAAA C
ATOM	1838	OG1	THR	188	28.943	5.365	89.016	1.00 89.33	AAAA O
ATOM	1840	CG2	THR	188	30.605	7.048	89.759	1.00 73.71	AAAA C
ATOM	1841	C	THR	188	29.802	8.583	87.429	1.00 67.52	AAAA C
ATOM	1842	O	THR	188	29.843	9.739	87.834	1.00 68.30	AAAA O
ATOM	1843	N	CYS	189	30.643	8.247	86.446	1.00 63.89	AAAA N
ATOM	1845	CA	CYS	189	31.583	9.116	85.817	1.00 57.29	AAAA C
ATOM	1846	C	CYS	189	30.951	10.331	85.195	1.00 57.70	AAAA C
ATOM	1847	O	CYS	189	31.648	11.327	85.017	1.00 57.56	AAAA O
ATOM	1848	CB	CYS	189	32.416	8.372	84.769	1.00 58.67	AAAA C
ATOM	1849	SG	CYS	189	33.347	7.001	85.535	1.00 53.46	AAAA S
ATOM	1850	N	GLY	190	29.689	10.322	84.806	1.00 56.91	AAAA N
ATOM	1852	CA	GLY	190	29.038	11.521	84.323	1.00 57.28	AAAA C
ATOM	1853	C	GLY	190	29.444	11.834	82.886	1.00 59.62	AAAA C
ATOM	1854	O	GLY	190	29.609	10.932	82.082	1.00 57.91	AAAA O
ATOM	1855	N	LYS	191	29.842	13.052	82.624	1.00 62.78	AAAA N
ATOM	1857	CA	LYS	191	30.359	13.520	81.364	1.00 67.72	AAAA C
ATOM	1858	CB	LYS	191	30.058	15.035	81.214	1.00 72.76	AAAA C
ATOM	1859	CG	LYS	191	28.568	15.288	81.002	1.00 84.69	AAAA C
ATOM	1860	CD	LYS	191	28.207	16.733	80.723	1.00 90.15	AAAA C
ATOM	1861	CE	LYS	191	26.713	16.806	80.471	1.00 91.83	AAAA C

ATOM	1962	HG	CYS	191	26.368	16.182	79.152	1.00	97.62	AAAA H
ATOM	1866	C	CYS	191	31.868	13.299	81.270	1.00	70.13	AAAA C
ATOM	1867	O	CYS	191	32.486	13.935	80.415	1.00	71.76	AAAA O
ATOM	1868	N	ARG	192	32.488	12.441	82.079	1.00	66.29	AAAA N
ATOM	1870	CA	ARG	192	33.885	12.171	82.044	1.00	59.95	AAAA C
ATOM	1871	CB	ARG	192	34.505	12.070	83.432	1.00	66.58	AAAA C
ATOM	1872	CG	ARG	192	34.670	13.400	84.131	1.00	71.59	AAAA C
ATOM	1873	CD	ARG	192	34.386	13.330	85.625	1.00	73.91	AAAA C
ATOM	1874	NE	ARG	192	35.622	13.280	86.377	1.00	85.74	AAAA N
ATOM	1876	CZ	ARG	192	35.968	12.407	87.330	1.00	90.67	AAAA C
ATOM	1877	NH1	ARG	192	35.026	11.486	87.600	1.00	88.49	AAAA N
ATOM	1880	NH2	ARG	192	37.162	12.463	87.950	1.00	72.95	AAAA N
ATOM	1883	C	ARG	192	34.221	10.851	81.337	1.00	58.83	AAAA C
ATOM	1884	O	ARG	192	33.336	10.007	81.176	1.00	55.13	AAAA O
ATOM	1885	N	ALA	193	35.521	10.795	80.968	1.00	50.19	AAAA N
ATOM	1887	CA	ALA	193	35.962	9.557	80.355	1.00	46.24	AAAA C
ATOM	1888	CB	ALA	193	37.167	9.921	79.541	1.00	45.15	AAAA C
ATOM	1889	C	ALA	193	36.221	8.525	81.451	1.00	48.97	AAAA C
ATOM	1890	O	ALA	193	36.220	8.908	82.616	1.00	44.80	AAAA O
ATOM	1891	N	CYS	194	36.544	7.304	81.065	1.00	50.30	AAAA N
ATOM	1893	CA	CYS	194	36.836	6.302	82.043	1.00	57.50	AAAA C
ATOM	1894	C	CYS	194	37.834	5.304	81.448	1.00	61.25	AAAA C
ATOM	1895	O	CYS	194	37.952	5.291	80.216	1.00	61.52	AAAA O
ATOM	1896	CB	CYS	194	35.510	5.741	82.504	1.00	57.96	AAAA C
ATOM	1897	SG	CYS	194	34.785	4.524	81.402	1.00	54.49	AAAA S
ATOM	1898	N	THR	195	38.422	4.499	82.311	1.00	58.51	AAAA N
ATOM	1900	CA	THR	195	39.462	3.584	81.913	1.00	57.42	AAAA C
ATOM	1901	CB	THR	195	40.237	3.142	83.188	1.00	65.73	AAAA C
ATOM	1902	OG1	THR	195	40.288	4.248	84.091	1.00	70.15	AAAA O
ATOM	1904	CG2	THR	195	41.684	2.864	82.745	1.00	77.91	AAAA C
ATOM	1905	C	THR	195	38.857	2.404	81.226	1.00	54.59	AAAA C
ATOM	1906	O	THR	195	37.633	2.315	81.318	1.00	58.75	AAAA O
ATOM	1907	N	GLU	196	39.610	1.408	80.882	1.00	55.95	AAAA N
ATOM	1909	CA	GLU	196	39.139	0.145	80.364	1.00	60.07	AAAA C
ATOM	1910	CB	GLU	196	40.395	-0.612	79.914	1.00	68.06	AAAA C
ATOM	1911	CG	GLU	196	40.479	-1.146	78.526	1.00	73.96	AAAA C
ATOM	1912	CD	GLU	196	39.235	-0.983	77.670	1.00	83.08	AAAA C
ATOM	1913	OE1	GLU	196	38.356	-1.884	77.687	1.00	81.19	AAAA O
ATOM	1914	OE2	GLU	196	39.060	0.041	76.939	1.00	82.10	AAAA O
ATOM	1915	C	GLU	196	38.382	-0.579	81.467	1.00	63.91	AAAA C
ATOM	1916	O	GLU	196	37.690	-1.537	81.159	1.00	63.51	AAAA O
ATOM	1917	N	ASN	197	38.666	-0.312	82.739	1.00	67.40	AAAA N
ATOM	1919	CA	ASN	197	38.025	-0.947	83.886	1.00	69.21	AAAA C
ATOM	1920	CB	ASN	197	39.021	-1.394	84.966	1.00	68.49	AAAA C
ATOM	1921	CG	ASN	197	39.722	-2.692	84.672	0.01	69.09	AAAA C
ATOM	1922	OD1	ASN	197	40.364	-3.273	85.551	0.01	69.04	AAAA O
ATOM	1923	ND2	ASN	197	39.622	-3.183	83.443	0.01	68.97	AAAA N
ATOM	1926	C	ASN	197	37.033	0.043	84.486	1.00	69.01	AAAA C
ATOM	1927	O	ASN	197	36.845	0.281	85.664	1.00	68.24	AAAA O
ATOM	1928	N	ASN	198	36.384	0.795	83.607	1.00	69.91	AAAA N
ATOM	1930	CA	ASN	198	35.356	1.734	84.048	1.00	68.48	AAAA C
ATOM	1931	CB	ASN	198	34.120	0.880	84.373	1.00	60.12	AAAA C
ATOM	1932	CG	ASN	198	33.806	0.095	83.102	1.00	69.29	AAAA C
ATOM	1933	OD1	ASN	198	33.475	0.654	82.054	1.00	73.20	AAAA O
ATOM	1934	ND2	ASN	198	33.980	-1.206	83.268	1.00	65.34	AAAA N
ATOM	1937	C	ASN	198	35.784	2.563	85.228	1.00	64.01	AAAA C
ATOM	1938	O	ASN	198	34.992	2.827	86.117	1.00	64.20	AAAA O
ATOM	1939	N	GLU	199	36.955	3.164	85.157	1.00	64.75	AAAA N
ATOM	1941	CA	GLU	199	37.342	4.054	86.255	1.00	64.64	AAAA C
ATOM	1942	CB	GLU	199	38.702	3.624	86.744	1.00	66.11	AAAA C
ATOM	1943	CG	GLU	199	38.846	3.717	88.233	1.00	77.15	AAAA C
ATOM	1944	CD	GLU	199	39.579	2.532	88.832	1.00	80.24	AAAA C
ATOM	1945	OE1	GLU	199	39.385	2.406	90.066	1.00	81.65	AAAA O
ATOM	1946	OE2	GLU	199	40.282	1.821	88.079	1.00	77.94	AAAA O
ATOM	1947	C	GLU	199	37.314	5.463	85.690	1.00	62.92	AAAA C
ATOM	1948	O	GLU	199	37.922	5.676	84.632	1.00	63.62	AAAA O
ATOM	1949	N	CYS	200	36.605	6.393	86.313	1.00	56.16	AAAA N
ATOM	1951	CA	CYS	200	36.600	7.721	85.740	1.00	55.11	AAAA C
ATOM	1952	C	CYS	200	37.978	8.315	85.521	1.00	57.77	AAAA C
ATOM	1953	O	CYS	200	38.884	8.058	86.300	1.00	63.79	AAAA O
ATOM	1954	CB	CYS	200	35.824	8.664	86.648	1.00	52.70	AAAA C
ATOM	1955	SG	CYS	200	34.196	8.100	87.098	1.00	55.85	AAAA S
ATOM	1956	N	CYS	201	38.124	9.192	84.540	1.00	54.50	AAAA N
ATOM	1958	CA	CYS	201	39.338	9.889	84.202	1.00	48.19	AAAA C
ATOM	1959	C	CYS	201	39.236	11.287	84.786	1.00	42.34	AAAA C
ATOM	1960	O	CYS	201	38.165	11.704	85.166	1.00	54.32	AAAA O
ATOM	1961	CB	CYS	201	39.590	10.070	82.695	1.00	40.90	AAAA C
ATOM	1962	SG	CYS	201	39.644	8.597	81.747	1.00	51.42	AAAA S
ATOM	1963	N	HIS	202	40.254	12.075	84.675	1.00	39.12	AAAA N
ATOM	1965	CA	HIS	202	40.290	13.461	85.128	1.00	41.55	AAAA C
ATOM	1966	C	HIS	202	39.284	14.184	84.289	1.00	46.59	AAAA C
ATOM	1967	O	HIS	202	39.176	13.851	83.103	1.00	51.64	AAAA O
ATOM	1968	CB	HIS	202	41.712	13.952	84.810	1.00	45.20	AAAA C
ATOM	1969	CG	HIS	202	41.996	15.330	85.267	1.00	38.71	AAAA C
ATOM	1970	ND1	HIS	202	41.501	16.404	84.550	1.00	51.32	AAAA N

ATOM	1971	CE1	HIS	202	41.887	17.528	85.178	1.00 47.62	AAAA C
ATOM	1972	CD2	HIS	202	42.665	15.813	86.340	1.00 39.59	AAAA C
ATOM	1973	NE2	HIS	202	42.563	17.207	86.258	1.00 43.48	AAAA N
ATOM	1975	N	PRO	203	38.738	15.293	84.711	1.00 47.74	AAAA N
ATOM	1976	CD	PRO	203	38.758	15.840	86.082	1.00 46.97	AAAA C
ATOM	1977	CA	PRO	203	37.780	15.987	83.879	1.00 46.44	AAAA C
ATOM	1978	CB	PRO	203	37.248	17.107	84.742	1.00 39.47	AAAA C
ATOM	1979	CG	PRO	203	38.131	17.210	85.910	1.00 43.37	AAAA C
ATOM	1980	C	PRO	203	38.440	16.519	82.607	1.00 53.27	AAAA C
ATOM	1981	O	PRO	203	37.698	17.045	81.731	1.00 53.16	AAAA O
ATOM	1982	N	GLU	204	39.792	16.535	82.561	1.00 50.34	AAAA N
ATOM	1984	CA	GLU	204	40.439	17.139	81.381	1.00 50.52	AAAA C
ATOM	1985	CB	GLU	204	41.727	17.891	81.804	1.00 48.58	AAAA C
ATOM	1986	CG	GLU	204	41.397	19.251	82.397	1.00 43.74	AAAA C
ATOM	1987	CD	GLU	204	40.778	20.282	81.501	1.00 55.26	AAAA C
ATOM	1988	OE1	GLU	204	40.766	20.344	80.248	1.00 64.04	AAAA O
ATOM	1989	OE2	GLU	204	40.226	21.198	82.141	1.00 57.66	AAAA O
ATOM	1990	C	GLU	204	40.718	16.084	80.319	1.00 45.71	AAAA C
ATOM	1991	O	GLU	204	41.238	16.405	79.251	1.00 46.56	AAAA O
ATOM	1992	N	CYS	205	40.612	14.830	80.735	1.00 42.05	AAAA N
ATOM	1994	CA	CYS	205	40.997	13.764	79.838	1.00 45.81	AAAA C
ATOM	1995	C	CYS	205	39.892	13.628	78.819	1.00 49.20	AAAA C
ATOM	1996	O	CYS	205	38.746	13.920	79.133	1.00 50.34	AAAA O
ATOM	1997	CB	CYS	205	41.288	12.491	80.572	1.00 51.55	AAAA C
ATOM	1998	SG	CYS	205	42.923	12.246	81.251	1.00 52.89	AAAA S
ATOM	1999	N	LEU	206	40.232	13.579	77.520	1.00 49.88	AAAA N
ATOM	2001	CA	LEU	206	39.169	13.446	76.533	1.00 41.49	AAAA C
ATOM	2002	CB	LEU	206	39.266	14.505	75.462	1.00 48.66	AAAA C
ATOM	2003	CG	LEU	206	38.274	14.365	74.305	1.00 47.45	AAAA C
ATOM	2004	CD1	LEU	206	36.879	14.243	74.895	1.00 45.79	AAAA C
ATOM	2005	CD2	LEU	206	38.331	15.599	73.420	1.00 50.71	AAAA C
ATOM	2006	C	LEU	206	39.310	12.109	75.912	1.00 38.44	AAAA C
ATOM	2007	O	LEU	206	40.400	11.568	75.813	1.00 36.59	AAAA O
ATOM	2008	N	GLY	207	38.264	11.359	75.681	1.00 42.41	AAAA N
ATOM	2010	CA	GLY	207	38.403	10.098	74.978	1.00 40.57	AAAA C
ATOM	2011	C	GLY	207	38.466	9.061	76.058	1.00 47.15	AAAA C
ATOM	2012	O	GLY	207	37.668	8.102	76.057	1.00 45.04	AAAA O
ATOM	2013	N	SER	208	39.622	9.079	76.760	1.00 50.36	AAAA N
ATOM	2015	CA	SER	208	39.832	7.898	77.660	1.00 48.27	AAAA C
ATOM	2016	CB	SER	208	39.909	6.631	76.787	1.00 35.77	AAAA C
ATOM	2017	OG	SER	208	40.600	5.597	77.461	1.00 61.34	AAAA O
ATOM	2019	C	SER	208	41.144	8.068	78.377	1.00 49.17	AAAA C
ATOM	2020	O	SER	208	41.781	9.084	78.163	1.00 48.24	AAAA O
ATOM	2021	N	CYS	209	41.599	7.123	79.189	1.00 52.04	AAAA N
ATOM	2023	CA	CYS	209	42.824	7.307	79.964	1.00 55.98	AAAA C
ATOM	2024	C	CYS	209	43.453	6.035	80.484	1.00 57.41	AAAA C
ATOM	2025	O	CYS	209	42.862	4.963	80.423	1.00 58.33	AAAA O
ATOM	2026	CB	CYS	209	42.629	8.258	81.146	1.00 52.51	AAAA C
ATOM	2027	SG	CYS	209	41.380	7.602	82.261	1.00 58.22	AAAA S
ATOM	2028	N	SER	210	44.734	6.145	80.883	1.00 59.37	AAAA N
ATOM	2030	CA	SER	210	45.506	4.950	81.318	1.00 58.10	AAAA C
ATOM	2031	CB	SER	210	47.022	5.083	81.105	1.00 55.07	AAAA C
ATOM	2032	OG	SER	210	47.546	6.204	81.818	1.00 64.49	AAAA O
ATOM	2034	C	SER	210	45.331	4.713	82.826	1.00 56.34	AAAA C
ATOM	2035	O	SER	210	45.529	3.614	83.326	1.00 54.42	AAAA O
ATOM	2036	N	ALA	211	45.105	5.806	83.548	1.00 52.79	AAAA N
ATOM	2038	CA	ALA	211	44.980	5.684	85.004	1.00 56.60	AAAA C
ATOM	2039	CB	ALA	211	46.333	5.926	85.649	1.00 63.41	AAAA C
ATOM	2040	C	ALA	211	43.962	6.747	85.395	1.00 56.58	AAAA C
ATOM	2041	O	ALA	211	43.957	7.792	84.711	1.00 50.78	AAAA O
ATOM	2042	N	PRO	212	43.117	6.416	86.359	1.00 55.93	AAAA N
ATOM	2043	CD	PRO	212	43.042	5.166	87.115	1.00 55.86	AAAA C
ATOM	2044	CA	PRO	212	41.951	7.257	86.575	1.00 55.50	AAAA C
ATOM	2045	CB	PRO	212	41.104	6.470	87.556	1.00 59.65	AAAA C
ATOM	2046	CG	PRO	212	42.021	5.483	88.175	1.00 54.56	AAAA C
ATOM	2047	C	PRO	212	42.409	8.535	87.177	1.00 53.64	AAAA C
ATOM	2048	O	PRO	212	43.611	8.725	87.393	1.00 57.46	AAAA O
ATOM	2049	N	ALA	213	41.537	9.492	87.347	1.00 53.87	AAAA N
ATOM	2051	CA	ALA	213	41.912	10.710	88.057	1.00 59.41	AAAA C
ATOM	2052	CB	ALA	213	41.783	10.255	89.541	1.00 66.40	AAAA C
ATOM	2053	C	ALA	213	43.289	11.300	87.907	1.00 61.40	AAAA C
ATOM	2054	O	ALA	213	43.728	12.202	88.652	1.00 60.03	AAAA O
ATOM	2055	N	ASN	214	44.068	10.999	86.899	1.00 64.80	AAAA N
ATOM	2057	CA	ASN	214	45.366	11.551	86.596	1.00 63.36	AAAA C
ATOM	2063	C	ASN	214	45.300	12.284	85.251	1.00 61.56	AAAA C
ATOM	2064	O	ASN	214	45.198	11.794	84.117	1.00 58.38	AAAA O
ATOM	2058	CB	ASN	214	46.336	10.379	86.608	1.00 67.32	AAAA C
ATOM	2059	CG	ASN	214	47.697	10.896	86.362	1.00 75.48	AAAA C
ATOM	2060	OD1	ASN	214	48.254	11.105	85.302	1.00 83.64	AAAA O
ATOM	2061	ND2	ASN	214	48.513	11.170	87.427	1.00 90.05	AAAA N
ATOM	2065	N	ASP	215	45.666	13.565	85.305	1.00 59.78	AAAA N
ATOM	2067	CA	ASP	215	45.618	14.432	84.143	1.00 56.47	AAAA C
ATOM	2068	CB	ASP	215	45.430	15.926	84.446	1.00 40.19	AAAA C
ATOM	2069	CG	ASP	215	46.671	16.543	84.986	1.00 56.36	AAAA C
ATOM	2070	OD1	ASP	215	46.590	17.699	85.473	1.00 56.17	AAAA O

ATOM	2071	OD2	ASP	215	47.766	15.926	84.941	1.00	60.51	AAAA O
ATOM	2072	C	ASP	215	46.818	14.315	83.221	1.00	53.78	AAAA C
ATOM	2073	O	ASP	215	46.998	15.148	82.322	1.00	53.58	AAAA O
ATOM	2074	N	THR	216	47.719	13.425	83.511	1.00	50.87	AAAA N
ATOM	2076	CA	THR	216	48.883	13.114	82.734	1.00	45.76	AAAA C
ATOM	2077	CB	THR	216	50.201	13.176	83.529	1.00	53.46	AAAA C
ATOM	2078	OG1	THR	216	50.403	11.977	84.335	1.00	45.14	AAAA O
ATOM	2080	CG2	THR	216	50.436	14.314	84.518	1.00	41.38	AAAA C
ATOM	2081	C	THR	216	48.681	11.712	82.158	1.00	48.34	AAAA C
ATOM	2082	O	THR	216	49.596	11.282	81.444	1.00	47.49	AAAA O
ATOM	2083	N	ALA	217	47.559	11.057	82.476	1.00	49.65	AAAA N
ATOM	2085	CA	ALA	217	47.259	9.760	81.845	1.00	51.83	AAAA C
ATOM	2086	CB	ALA	217	46.908	8.775	82.943	1.00	52.62	AAAA C
ATOM	2087	C	ALA	217	46.207	9.747	80.709	1.00	50.60	AAAA C
ATOM	2088	O	ALA	217	45.775	8.632	80.335	1.00	49.13	AAAA O
ATOM	2089	N	CYS	218	45.744	10.905	80.226	1.00	43.56	AAAA N
ATOM	2091	CA	CYS	218	44.802	11.030	79.157	1.00	48.09	AAAA C
ATOM	2092	C	CYS	218	45.166	10.331	77.869	1.00	47.06	AAAA C
ATOM	2093	O	CYS	218	46.300	9.967	77.642	1.00	55.57	AAAA O
ATOM	2094	CB	CYS	218	44.536	12.501	78.775	1.00	51.54	AAAA C
ATOM	2095	SG	CYS	218	44.256	13.494	80.302	1.00	56.98	AAAA S
ATOM	2096	N	VAL	219	44.226	10.085	76.978	1.00	43.40	AAAA N
ATOM	2098	CA	VAL	219	44.575	9.547	75.654	1.00	35.22	AAAA C
ATOM	2099	CB	VAL	219	43.693	8.427	75.242	1.00	32.26	AAAA C
ATOM	2100	CG1	VAL	219	43.952	7.873	73.886	1.00	36.19	AAAA C
ATOM	2101	CG2	VAL	219	43.811	7.144	76.071	1.00	45.51	AAAA C
ATOM	2102	C	VAL	219	44.453	10.750	74.735	1.00	32.06	AAAA C
ATOM	2103	O	VAL	219	45.303	10.897	73.874	1.00	42.27	AAAA O
ATOM	2104	N	ALA	220	43.729	11.759	75.187	1.00	24.24	AAAA N
ATOM	2106	CA	ALA	220	43.630	12.985	74.385	1.00	27.99	AAAA C
ATOM	2107	CB	ALA	220	42.536	12.919	73.331	1.00	28.42	AAAA C
ATOM	2108	C	ALA	220	43.292	14.071	75.390	1.00	29.21	AAAA C
ATOM	2109	O	ALA	220	42.846	13.604	76.455	1.00	37.88	AAAA O
ATOM	2110	N	CYS	221	43.285	15.334	75.058	1.00	30.27	AAAA N
ATOM	2112	CA	CYS	221	42.753	16.382	75.875	1.00	35.55	AAAA C
ATOM	2113	C	CYS	221	41.460	17.055	75.452	1.00	47.06	AAAA C
ATOM	2114	O	CYS	221	41.265	17.598	74.368	1.00	49.57	AAAA O
ATOM	2115	CB	CYS	221	43.804	17.478	76.063	1.00	47.45	AAAA C
ATOM	2116	SG	CYS	221	45.494	16.935	76.538	1.00	47.06	AAAA S
ATOM	2117	N	ARG	222	40.503	17.133	76.396	1.00	51.47	AAAA N
ATOM	2119	CA	ARG	222	39.281	17.906	76.338	1.00	51.86	AAAA C
ATOM	2120	CB	ARG	222	38.647	18.074	77.712	1.00	54.53	AAAA C
ATOM	2121	CG	ARG	222	37.314	18.687	77.854	1.00	45.56	AAAA C
ATOM	2122	CD	ARG	222	36.538	18.338	79.087	1.00	54.45	AAAA C
ATOM	2123	NE	ARG	222	36.272	16.947	79.269	1.00	65.53	AAAA N
ATOM	2125	CZ	ARG	222	35.534	16.080	78.617	1.00	67.60	AAAA C
ATOM	2126	NH1	ARG	222	34.925	16.599	77.533	1.00	70.26	AAAA N
ATOM	2129	NH2	ARG	222	35.342	14.780	78.901	1.00	54.11	AAAA N
ATOM	2132	C	ARG	222	39.562	19.286	75.740	1.00	50.66	AAAA C
ATOM	2133	O	ARG	222	38.737	19.845	75.009	1.00	58.34	AAAA O
ATOM	2134	N	HIS	223	40.556	19.981	76.190	1.00	45.65	AAAA N
ATOM	2136	CA	HIS	223	40.988	21.291	75.921	1.00	46.93	AAAA C
ATOM	2137	CB	HIS	223	41.057	22.251	77.011	1.00	49.51	AAAA C
ATOM	2138	CG	HIS	223	39.710	22.344	77.617	1.00	58.83	AAAA C
ATOM	2139	CD2	HIS	223	38.820	23.360	77.556	1.00	61.08	AAAA C
ATOM	2140	ND1	HIS	223	39.082	21.388	78.425	1.00	63.28	AAAA N
ATOM	2142	CE1	HIS	223	37.881	21.815	78.759	1.00	58.01	AAAA C
ATOM	2143	NE2	HIS	223	37.681	23.010	78.230	1.00	48.56	AAAA N
ATOM	2145	C	HIS	223	42.363	21.260	75.122	1.00	50.78	AAAA C
ATOM	2146	O	HIS	223	42.506	20.753	74.003	1.00	47.43	AAAA O
ATOM	2147	N	TYR	224	43.359	21.847	75.769	1.00	49.20	AAAA N
ATOM	2149	CA	TYR	224	44.712	21.992	75.259	1.00	48.17	AAAA C
ATOM	2150	CB	TYR	224	45.144	23.430	75.426	1.00	44.07	AAAA C
ATOM	2151	CG	TYR	224	44.318	24.234	74.417	1.00	51.77	AAAA C
ATOM	2152	CD1	TYR	224	43.193	24.869	74.904	1.00	48.94	AAAA C
ATOM	2153	CE1	TYR	224	42.401	25.633	74.089	1.00	48.41	AAAA C
ATOM	2154	CD2	TYR	224	44.623	24.358	73.065	1.00	54.82	AAAA C
ATOM	2155	CE2	TYR	224	43.847	25.131	72.233	1.00	56.09	AAAA C
ATOM	2156	CZ	TYR	224	42.739	25.745	72.766	1.00	54.23	AAAA C
ATOM	2157	OH	TYR	224	41.915	26.522	72.017	1.00	61.70	AAAA O
ATOM	2159	C	TYR	224	45.725	21.095	75.892	1.00	48.19	AAAA C
ATOM	2160	O	TYR	224	45.776	20.913	77.111	1.00	55.75	AAAA O
ATOM	2161	N	TYR	225	46.584	20.514	75.077	1.00	48.79	AAAA N
ATOM	2163	CA	TYR	225	47.655	19.653	75.555	1.00	43.02	AAAA C
ATOM	2164	CB	TYR	225	48.020	18.639	74.548	1.00	42.32	AAAA C
ATOM	2165	CG	TYR	225	49.286	17.926	74.954	1.00	46.95	AAAA C
ATOM	2166	CD1	TYR	225	49.299	16.858	75.817	1.00	43.57	AAAA C
ATOM	2167	CE1	TYR	225	50.450	16.221	76.173	1.00	47.26	AAAA C
ATOM	2168	CD2	TYR	225	50.487	18.407	74.421	1.00	52.82	AAAA C
ATOM	2169	CE2	TYR	225	51.656	17.791	74.781	1.00	53.94	AAAA C
ATOM	2170	CZ	TYR	225	51.639	16.707	75.644	1.00	52.31	AAAA C
ATOM	2171	OH	TYR	225	52.806	16.196	75.995	1.00	50.71	AAAA O
ATOM	2173	C	TYR	225	48.872	20.507	75.793	1.00	47.13	AAAA C
ATOM	2174	O	TYR	225	49.089	21.514	75.150	1.00	53.97	AAAA O
ATOM	2175	N	TYR	226	49.634	20.253	76.821	1.00	56.84	AAAA N

ATOM	2177	CA	TYR	226	50.811	21.001	77.172	1.00	56.83	AAAA C
ATOM	2178	CB	TYR	226	50.455	22.343	77.785	1.00	59.51	AAAA C
ATOM	2179	CG	TYR	226	51.741	23.126	77.941	1.00	65.45	AAAA C
ATOM	2180	CD1	TYR	226	52.121	23.557	79.197	1.00	69.12	AAAA C
ATOM	2181	CE1	TYR	226	53.289	24.275	79.400	1.00	70.77	AAAA C
ATOM	2182	CD2	TYR	226	52.580	23.409	76.864	1.00	69.38	AAAA C
ATOM	2183	CE2	TYR	226	53.758	24.118	77.020	1.00	70.94	AAAA C
ATOM	2184	CZ	TYR	226	54.099	24.549	78.301	1.00	72.96	AAAA C
ATOM	2185	OH	TYR	226	55.267	25.254	78.435	1.00	70.84	AAAA O
ATOM	2187	C	TYR	226	51.784	20.356	78.165	1.00	57.55	AAAA C
ATOM	2188	O	TYR	226	51.492	20.133	79.350	1.00	56.90	AAAA O
ATOM	2189	N	ALA	227	52.978	20.080	77.642	1.00	53.82	AAAA N
ATOM	2191	CA	ALA	227	54.061	19.557	78.440	1.00	51.82	AAAA C
ATOM	2192	CB	ALA	227	54.528	20.620	79.428	1.00	55.81	AAAA C
ATOM	2193	C	ALA	227	53.600	18.309	79.170	1.00	53.56	AAAA C
ATOM	2194	O	ALA	227	53.663	18.218	80.413	1.00	49.63	AAAA O
ATOM	2195	N	GLY	228	53.076	17.360	78.393	1.00	50.68	AAAA N
ATOM	2197	CA	GLY	228	52.585	16.135	79.028	1.00	49.02	AAAA C
ATOM	2198	C	GLY	228	51.312	16.330	79.861	1.00	51.61	AAAA C
ATOM	2199	O	GLY	228	51.028	15.538	80.776	1.00	51.10	AAAA O
ATOM	2200	N	VAL	229	50.643	17.495	79.791	1.00	47.09	AAAA N
ATOM	2202	CA	VAL	229	49.489	17.671	80.635	1.00	51.11	AAAA C
ATOM	2203	CB	VAL	229	49.908	18.610	81.774	1.00	56.52	AAAA C
ATOM	2204	CG1	VAL	229	48.627	18.896	82.566	1.00	38.39	AAAA C
ATOM	2205	CG2	VAL	229	51.002	18.035	82.682	1.00	50.16	AAAA C
ATOM	2206	C	VAL	229	48.255	18.173	79.873	1.00	51.37	AAAA C
ATOM	2207	O	VAL	229	48.344	19.279	79.309	1.00	53.71	AAAA O
ATOM	2208	N	CYS	230	47.100	17.518	80.036	1.00	42.21	AAAA N
ATOM	2210	CA	CYS	230	45.981	18.117	79.471	1.00	40.32	AAAA C
ATOM	2211	C	CYS	230	45.456	19.350	80.228	1.00	38.42	AAAA C
ATOM	2212	O	CYS	230	44.964	19.248	81.321	1.00	41.62	AAAA O
ATOM	2213	CB	CYS	230	44.746	17.132	79.370	1.00	31.54	AAAA C
ATOM	2214	SG	CYS	230	45.149	15.753	78.266	1.00	43.61	AAAA S
ATOM	2215	N	VAL	231	45.637	20.534	79.731	1.00	39.83	AAAA N
ATOM	2217	CA	VAL	231	45.445	21.769	80.462	1.00	46.57	AAAA C
ATOM	2218	CB	VAL	231	46.618	22.736	80.088	1.00	50.99	AAAA C
ATOM	2219	CG1	VAL	231	46.798	23.878	81.053	1.00	50.41	AAAA C
ATOM	2220	CG2	VAL	231	47.838	21.913	80.506	1.00	44.95	AAAA C
ATOM	2221	C	VAL	231	44.111	22.321	80.057	1.00	52.59	AAAA C
ATOM	2222	O	VAL	231	43.599	22.183	78.936	1.00	55.30	AAAA O
ATOM	2223	N	PRO	232	43.482	23.105	80.913	1.00	54.28	AAAA N
ATOM	2224	CD	PRO	232	43.830	23.385	82.320	1.00	54.25	AAAA C
ATOM	2225	CA	PRO	232	42.153	23.625	80.575	1.00	54.39	AAAA C
ATOM	2226	CB	PRO	232	41.537	23.877	81.928	1.00	53.73	AAAA C
ATOM	2227	CG	PRO	232	42.683	24.287	82.765	1.00	55.00	AAAA C
ATOM	2228	C	PRO	232	42.361	24.913	79.795	1.00	56.37	AAAA C
ATOM	2229	O	PRO	232	41.498	25.482	79.137	1.00	55.79	AAAA O
ATOM	2230	N	ALA	233	43.615	25.400	79.901	1.00	54.76	AAAA N
ATOM	2232	CA	ALA	233	43.998	26.569	79.124	1.00	49.93	AAAA C
ATOM	2233	CB	ALA	233	43.440	27.807	79.746	1.00	35.43	AAAA C
ATOM	2234	C	ALA	233	45.502	26.662	78.974	1.00	49.79	AAAA C
ATOM	2235	O	ALA	233	46.195	25.879	79.616	1.00	51.41	AAAA O
ATOM	2236	N	CYS	234	45.984	27.508	78.072	1.00	45.07	AAAA N
ATOM	2238	CA	CYS	234	47.430	27.518	77.907	1.00	48.63	AAAA C
ATOM	2239	C	CYS	234	48.001	28.340	79.076	1.00	50.93	AAAA C
ATOM	2240	O	CYS	234	47.650	29.513	79.250	1.00	47.57	AAAA O
ATOM	2241	CB	CYS	234	47.816	28.034	76.511	1.00	43.10	AAAA C
ATOM	2242	SG	CYS	234	47.608	26.789	75.226	1.00	43.04	AAAA S
ATOM	2243	N	PRO	235	49.127	27.853	79.599	1.00	49.55	AAAA N
ATOM	2244	CD	PRO	235	49.692	26.557	79.207	1.00	48.75	AAAA C
ATOM	2245	CA	PRO	235	49.911	28.569	80.599	1.00	51.69	AAAA C
ATOM	2246	CB	PRO	235	50.984	27.581	80.975	1.00	50.80	AAAA C
ATOM	2247	CG	PRO	235	50.912	26.417	80.077	1.00	50.06	AAAA C
ATOM	2248	C	PRO	235	50.487	29.852	80.050	1.00	57.11	AAAA C
ATOM	2249	O	PRO	235	50.848	29.957	78.870	1.00	59.60	AAAA O
ATOM	2250	N	PRO	236	50.676	30.875	80.887	1.00	59.85	AAAA N
ATOM	2251	CD	PRO	236	50.405	30.822	82.363	1.00	55.85	AAAA C
ATOM	2252	CA	PRO	236	51.323	32.143	80.493	1.00	52.27	AAAA C
ATOM	2253	CB	PRO	236	51.695	32.814	81.826	1.00	53.62	AAAA C
ATOM	2254	CG	PRO	236	50.652	32.277	82.754	1.00	56.73	AAAA C
ATOM	2255	C	PRO	236	52.545	31.886	79.671	1.00	44.21	AAAA C
ATOM	2256	O	PRO	236	53.219	30.892	79.928	1.00	43.40	AAAA O
ATOM	2257	N	ASN	237	52.837	32.757	78.716	1.00	46.54	AAAA N
ATOM	2259	CA	ASN	237	53.895	32.623	77.716	1.00	45.94	AAAA C
ATOM	2260	CB	ASN	237	55.259	32.653	78.456	1.00	58.65	AAAA C
ATOM	2261	CG	ASN	237	55.357	33.855	79.371	1.00	58.51	AAAA C
ATOM	2262	OD1	ASN	237	56.044	33.783	80.379	1.00	72.25	AAAA O
ATOM	2263	ND2	ASN	237	54.631	34.910	79.051	1.00	62.99	AAAA N
ATOM	2266	C	ASN	237	53.897	31.425	76.788	1.00	46.87	AAAA C
ATOM	2267	O	ASN	237	54.962	30.935	76.326	1.00	54.50	AAAA O
ATOM	2268	N	THR	238	52.617	30.657	76.692	1.00	42.91	AAAA N
ATOM	2270	CA	THR	238	52.617	29.567	75.780	1.00	40.20	AAAA C
ATOM	2271	CB	THR	238	52.481	28.248	76.466	1.00	42.62	AAAA C
ATOM	2272	OG1	THR	238	51.227	28.343	77.237	1.00	50.88	AAAA O
ATOM	2274	CG2	THR	238	53.552	27.986	77.424	1.00	34.84	AAAA C

ATOM	2275	C	THR	238	51.279	29.875	75.078	1.00 42.59	AAAA C
ATOM	2276	O	THR	238	50.669	30.864	75.509	1.00 42.51	AAAA O
ATOM	2277	N	TYR	239	51.051	29.488	73.832	1.00 42.62	AAAA N
ATOM	2279	CA	TYR	239	49.949	29.959	73.024	1.00 41.87	AAAA C
ATOM	2280	CB	TYR	239	50.457	30.907	71.931	1.00 44.86	AAAA C
ATOM	2281	CG	TYR	239	51.099	32.125	72.564	1.00 42.05	AAAA C
ATOM	2282	CD1	TYR	239	52.467	32.086	72.815	1.00 39.41	AAAA C
ATOM	2283	CE1	TYR	239	53.092	33.152	73.415	1.00 43.27	AAAA C
ATOM	2284	CD2	TYR	239	50.376	33.230	72.923	1.00 44.15	AAAA C
ATOM	2285	CE2	TYR	239	50.972	34.310	73.536	1.00 46.22	AAAA C
ATOM	2286	CZ	TYR	239	52.339	34.243	73.779	1.00 50.49	AAAA C
ATOM	2287	OH	TYR	239	53.013	35.289	74.387	1.00 55.47	AAAA O
ATOM	2289	C	TYR	239	49.232	28.813	72.315	1.00 45.54	AAAA C
ATOM	2290	O	TYR	239	49.922	27.810	72.021	1.00 46.66	AAAA O
ATOM	2291	N	ARG	240	47.895	28.990	72.126	1.00 40.62	AAAA N
ATOM	2293	CA	ARG	240	47.177	27.892	71.426	1.00 38.78	AAAA C
ATOM	2294	CB	ARG	240	45.675	28.127	71.452	1.00 39.77	AAAA C
ATOM	2295	CG	ARG	240	45.116	28.944	72.588	1.00 43.37	AAAA C
ATOM	2296	CD	ARG	240	43.573	28.957	72.683	1.00 38.60	AAAA C
ATOM	2297	NE	ARG	240	43.114	29.683	71.455	1.00 53.98	AAAA N
ATOM	2299	CZ	ARG	240	43.123	31.015	71.530	1.00 48.07	AAAA C
ATOM	2300	NH1	ARG	240	43.513	31.562	72.668	1.00 47.65	AAAA N
ATOM	2303	NH2	ARG	240	42.788	31.778	70.533	1.00 51.03	AAAA N
ATOM	2306	C	ARG	240	47.627	27.737	69.979	1.00 31.72	AAAA C
ATOM	2307	O	ARG	240	47.937	28.730	69.302	1.00 32.37	AAAA O
ATOM	2308	N	PHE	241	47.779	26.542	69.549	1.00 27.95	AAAA N
ATOM	2310	CA	PHE	241	48.182	26.269	68.183	1.00 30.41	AAAA C
ATOM	2311	CB	PHE	241	49.678	25.940	68.151	1.00 34.83	AAAA C
ATOM	2312	CG	PHE	241	50.235	25.653	66.773	1.00 26.84	AAAA C
ATOM	2313	CD1	PHE	241	50.165	26.567	65.753	1.00 25.31	AAAA C
ATOM	2314	CD2	PHE	241	50.785	24.417	66.573	1.00 27.38	AAAA C
ATOM	2315	CE1	PHE	241	50.676	26.232	64.509	1.00 37.24	AAAA C
ATOM	2316	CE2	PHE	241	51.294	24.101	65.320	1.00 38.45	AAAA C
ATOM	2317	CZ	PHE	241	51.281	25.010	64.281	1.00 21.17	AAAA C
ATOM	2318	C	PHE	241	47.382	25.089	67.621	1.00 35.77	AAAA C
ATOM	2319	O	PHE	241	47.543	24.013	68.186	1.00 36.77	AAAA O
ATOM	2320	N	GLU	242	46.738	25.301	66.468	1.00 32.30	AAAA N
ATOM	2322	CA	GLU	242	45.964	24.269	65.805	1.00 35.43	AAAA C
ATOM	2323	CB	GLU	242	46.953	23.144	65.472	1.00 37.98	AAAA C
ATOM	2324	CG	GLU	242	47.867	23.415	64.314	1.00 38.63	AAAA C
ATOM	2325	CD	GLU	242	47.207	23.965	63.075	1.00 39.27	AAAA C
ATOM	2326	OE1	GLU	242	46.380	23.205	62.517	1.00 42.79	AAAA O
ATOM	2327	OE2	GLU	242	47.354	25.109	62.626	1.00 36.36	AAAA O
ATOM	2328	C	GLU	242	44.752	23.771	66.600	1.00 34.36	AAAA C
ATOM	2329	O	GLU	242	44.390	22.611	66.511	1.00 28.53	AAAA O
ATOM	2330	N	GLY	243	44.135	24.589	67.449	1.00 36.94	AAAA N
ATOM	2332	CA	GLY	243	43.048	24.154	68.303	1.00 34.57	AAAA C
ATOM	2333	C	GLY	243	43.428	23.107	69.319	1.00 37.76	AAAA C
ATOM	2334	O	GLY	243	42.474	22.473	69.746	1.00 43.00	AAAA O
ATOM	2335	N	TRP	244	44.637	22.636	69.611	1.00 39.53	AAAA N
ATOM	2337	CA	TRP	244	44.797	21.536	70.566	1.00 40.85	AAAA C
ATOM	2338	CB	TRP	244	44.774	20.271	69.764	1.00 26.76	AAAA C
ATOM	2339	CG	TRP	244	46.012	19.885	69.028	1.00 43.19	AAAA C
ATOM	2340	CD2	TRP	244	47.019	18.983	69.498	1.00 39.55	AAAA C
ATOM	2341	CE2	TRP	244	47.998	18.906	68.489	1.00 36.50	AAAA C
ATOM	2342	CE3	TRP	244	47.186	18.254	70.692	1.00 32.18	AAAA C
ATOM	2343	CD1	TRP	244	46.424	20.308	67.779	1.00 43.37	AAAA C
ATOM	2344	NE1	TRP	244	47.595	19.727	67.469	1.00 38.89	AAAA N
ATOM	2346	CZ2	TRP	244	49.150	18.128	68.620	1.00 39.01	AAAA C
ATOM	2347	CZ3	TRP	244	48.336	17.478	70.815	1.00 43.98	AAAA C
ATOM	2348	CH2	TRP	244	49.322	17.425	69.784	1.00 42.50	AAAA C
ATOM	2349	C	TRP	244	45.998	21.517	71.509	1.00 42.98	AAAA C
ATOM	2350	O	TRP	244	46.253	20.501	72.146	1.00 42.70	AAAA O
ATOM	2351	N	ARG	245	46.888	22.485	71.435	1.00 44.16	AAAA N
ATOM	2353	CA	ARG	245	48.168	22.472	72.095	1.00 46.47	AAAA C
ATOM	2354	CB	ARG	245	49.203	21.602	71.367	1.00 47.30	AAAA C
ATOM	2355	CG	ARG	245	49.985	22.309	70.203	1.00 48.97	AAAA C
ATOM	2356	CD	ARG	245	51.129	21.552	69.819	1.00 39.28	AAAA C
ATOM	2357	NE	ARG	245	51.586	21.665	68.444	1.00 50.86	AAAA N
ATOM	2359	CZ	ARG	245	52.629	21.044	67.895	1.00 46.73	AAAA C
ATOM	2360	NH1	ARG	245	53.344	20.236	68.653	1.00 50.15	AAAA N
ATOM	2363	NH2	ARG	245	53.072	21.126	66.638	1.00 41.69	AAAA N
ATOM	2366	C	ARG	245	48.771	23.863	72.271	1.00 46.01	AAAA C
ATOM	2367	O	ARG	245	48.394	24.793	71.541	1.00 47.44	AAAA O
ATOM	2368	N	CYS	246	49.625	23.881	73.317	1.00 42.08	AAAA N
ATOM	2370	CA	CYS	246	50.246	25.199	73.628	1.00 43.48	AAAA C
ATOM	2371	C	CYS	246	51.695	25.217	73.183	1.00 43.38	AAAA C
ATOM	2372	O	CYS	246	52.476	24.239	73.320	1.00 42.51	AAAA O
ATOM	2373	CB	CYS	246	50.102	25.392	75.138	1.00 48.91	AAAA C
ATOM	2374	SG	CYS	246	48.386	25.049	75.797	1.00 43.68	AAAA S
ATOM	2375	N	VAL	247	52.121	26.288	72.564	1.00 41.21	AAAA N
ATOM	2377	CA	VAL	247	53.417	26.468	71.982	1.00 36.51	AAAA C
ATOM	2378	CB	VAL	247	53.569	26.357	70.444	1.00 36.87	AAAA C
ATOM	2379	CG1	VAL	247	53.089	24.988	70.024	1.00 32.71	AAAA C
ATOM	2380	CG2	VAL	247	53.129	27.602	69.729	1.00 28.20	AAAA C

ATOM	2381	C	VAL	247	53.969	27.812	72.373	1.00 39.37	AAAA C
ATOM	2382	O	VAL	247	53.230	28.770	72.540	1.00 38.80	AAAA O
ATOM	2383	N	ASP	248	55.291	27.820	72.711	1.00 45.21	AAAA N
ATOM	2385	CA	ASP	248	55.895	29.115	73.098	1.00 40.19	AAAA C
ATOM	2386	CB	ASP	248	57.091	28.946	73.953	1.00 42.63	AAAA C
ATOM	2387	CG	ASP	248	58.126	27.997	73.394	1.00 58.81	AAAA C
ATOM	2388	OD1	ASP	248	59.067	27.795	74.187	1.00 53.06	AAAA O
ATOM	2389	OD2	ASP	248	58.167	27.395	72.313	1.00 69.51	AAAA O
ATOM	2390	C	ASP	248	56.315	29.883	71.839	1.00 36.99	AAAA C
ATOM	2391	O	ASP	248	56.292	29.288	70.772	1.00 39.70	AAAA O
ATOM	2392	N	ARG	249	56.545	31.163	71.918	1.00 30.72	AAAA N
ATOM	2394	CA	ARG	249	56.950	32.057	70.906	1.00 36.17	AAAA C
ATOM	2395	CB	ARG	249	57.223	33.485	71.491	1.00 21.29	AAAA C
ATOM	2396	CG	ARG	249	57.594	34.424	70.326	1.00 24.96	AAAA C
ATOM	2397	CD	ARG	249	57.814	35.811	70.843	1.00 21.23	AAAA C
ATOM	2398	NE	ARG	249	56.658	36.150	71.689	1.00 39.75	AAAA N
ATOM	2400	CZ	ARG	249	55.632	36.823	71.101	1.00 39.35	AAAA C
ATOM	2401	NH1	ARG	249	55.642	37.118	69.801	1.00 25.41	AAAA N
ATOM	2404	NH2	ARG	249	54.641	37.118	71.946	1.00 44.04	AAAA N
ATOM	2407	C	ARG	249	58.134	31.685	70.010	1.00 40.63	AAAA C
ATOM	2408	O	ARG	249	58.086	31.923	68.797	1.00 44.79	AAAA O
ATOM	2409	N	ASP	250	59.149	30.974	70.468	1.00 41.87	AAAA N
ATOM	2411	CA	ASP	250	60.287	30.739	69.606	1.00 46.90	AAAA C
ATOM	2412	CB	ASP	250	61.740	30.726	70.154	1.00 53.11	AAAA C
ATOM	2413	CG	ASP	250	62.421	32.122	70.081	1.00 71.49	AAAA C
ATOM	2414	OD1	ASP	250	63.124	32.682	69.176	1.00 58.53	AAAA O
ATOM	2415	OD2	ASP	250	62.272	32.928	71.071	1.00 70.30	AAAA O
ATOM	2416	C	ASP	250	59.881	29.536	68.771	1.00 41.22	AAAA C
ATOM	2417	O	ASP	250	60.291	29.443	67.616	1.00 39.06	AAAA O
ATOM	2418	N	PHE	251	59.116	28.609	69.299	1.00 36.13	AAAA N
ATOM	2420	CA	PHE	251	58.457	27.601	68.489	1.00 34.88	AAAA C
ATOM	2421	CB	PHE	251	57.468	26.746	69.256	1.00 29.82	AAAA C
ATOM	2422	CG	PHE	251	56.701	25.801	68.385	1.00 41.50	AAAA C
ATOM	2423	CD1	PHE	251	57.101	24.479	68.263	1.00 30.66	AAAA C
ATOM	2424	CD2	PHE	251	55.559	26.213	67.686	1.00 37.78	AAAA C
ATOM	2425	CE1	PHE	251	56.414	23.597	67.424	1.00 29.30	AAAA C
ATOM	2426	CE2	PHE	251	54.847	25.372	66.856	1.00 36.09	AAAA C
ATOM	2427	CZ	PHE	251	55.294	24.070	66.715	1.00 36.21	AAAA C
ATOM	2428	C	PHE	251	57.624	28.290	67.338	1.00 39.28	AAAA C
ATOM	2429	O	PHE	251	57.811	28.010	66.144	1.00 30.27	AAAA O
ATOM	2430	N	CYS	252	56.734	29.225	67.713	1.00 35.13	AAAA N
ATOM	2432	CA	CYS	252	55.895	29.870	66.728	1.00 38.80	AAAA C
ATOM	2433	C	CYS	252	56.827	30.598	65.747	1.00 44.73	AAAA C
ATOM	2434	O	CYS	252	56.552	30.534	64.536	1.00 43.20	AAAA O
ATOM	2435	CB	CYS	252	54.903	30.778	67.379	1.00 35.65	AAAA C
ATOM	2436	SG	CYS	252	53.562	31.544	66.459	1.00 39.03	AAAA S
ATOM	2437	N	ALA	253	57.872	31.256	66.285	1.00 41.53	AAAA N
ATOM	2439	CA	ALA	253	58.687	32.071	65.415	1.00 40.39	AAAA C
ATOM	2440	CB	ALA	253	59.529	33.088	66.172	1.00 36.07	AAAA C
ATOM	2441	C	ALA	253	59.551	31.167	64.539	1.00 42.88	AAAA C
ATOM	2442	O	ALA	253	60.147	31.735	63.640	1.00 47.42	AAAA O
ATOM	2443	N	ASN	254	59.657	29.859	64.700	1.00 38.75	AAAA N
ATOM	2445	CA	ASN	254	60.546	29.073	63.929	1.00 42.94	AAAA C
ATOM	2446	CB	ASN	254	61.667	28.497	64.847	1.00 48.09	AAAA C
ATOM	2447	CG	ASN	254	62.696	29.635	65.031	1.00 49.94	AAAA C
ATOM	2448	OD1	ASN	254	63.468	29.840	64.081	1.00 61.38	AAAA O
ATOM	2449	ND2	ASN	254	62.607	30.321	66.144	1.00 48.38	AAAA N
ATOM	2452	C	ASN	254	59.907	27.959	63.135	1.00 53.72	AAAA C
ATOM	2453	O	ASN	254	60.552	26.965	62.804	1.00 51.19	AAAA O
ATOM	2454	N	ILE	255	58.612	28.136	62.766	1.00 57.77	AAAA N
ATOM	2456	CA	ILE	255	57.828	27.107	62.134	1.00 53.28	AAAA C
ATOM	2457	CB	ILE	255	56.329	27.322	62.304	1.00 50.41	AAAA C
ATOM	2458	CG2	ILE	255	55.477	26.595	61.246	1.00 51.95	AAAA C
ATOM	2459	CG1	ILE	255	55.778	26.675	63.553	1.00 40.59	AAAA C
ATOM	2460	CD1	ILE	255	54.479	27.317	64.006	1.00 38.97	AAAA C
ATOM	2461	C	ILE	255	58.127	26.886	60.651	1.00 52.62	AAAA C
ATOM	2462	O	ILE	255	58.196	25.709	60.252	1.00 53.96	AAAA O
ATOM	2463	N	LEU	256	58.290	27.960	59.918	1.00 49.96	AAAA N
ATOM	2465	CA	LEU	256	58.680	27.764	58.516	1.00 63.68	AAAA C
ATOM	2466	CB	LEU	256	58.175	29.012	57.799	1.00 56.80	AAAA C
ATOM	2467	CG	LEU	256	56.671	29.196	57.864	1.00 59.11	AAAA C
ATOM	2468	CD1	LEU	256	56.310	30.654	57.645	1.00 43.31	AAAA C
ATOM	2469	CD2	LEU	256	55.965	28.222	56.928	1.00 55.88	AAAA C
ATOM	2470	C	LEU	256	60.193	27.622	58.355	1.00 66.23	AAAA C
ATOM	2471	O	LEU	256	60.691	27.511	57.245	1.00 70.29	AAAA O
ATOM	2472	N	SER	257	60.942	27.559	59.430	1.00 64.61	AAAA N
ATOM	2474	CA	SER	257	62.352	27.529	59.534	1.00 69.23	AAAA C
ATOM	2475	CB	SER	257	62.924	27.318	60.955	1.00 62.45	AAAA C
ATOM	2476	OG	SER	257	63.381	25.980	61.074	1.00 56.18	AAAA O
ATOM	2478	C	SER	257	62.973	26.497	58.610	1.00 70.77	AAAA C
ATOM	2479	O	SER	257	64.127	26.731	58.246	1.00 72.50	AAAA O
ATOM	2480	N	ALA	258	62.322	25.399	58.320	1.00 74.61	AAAA N
ATOM	2482	CA	ALA	258	62.933	24.488	57.343	1.00 76.34	AAAA C
ATOM	2483	CB	ALA	258	62.570	23.039	57.584	1.00 80.82	AAAA C
ATOM	2484	C	ALA	258	62.663	24.964	55.921	1.00 78.21	AAAA C

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ATOM  2485  O   ALA  259      62.880  24.139  55.029  1.00 79.60      AAAA O
ATOM  2486  N   GLU  259      62.069  26.109  55.651  1.00 79.05      AAAA N
ATOM  2488  CA  GLU  259      61.742  26.621  54.349  1.00 83.84      AAAA C
ATOM  2489  CB  GLU  259      60.226  26.457  54.135  1.00 86.99      AAAA C
ATOM  2490  CG  GLU  259      59.687  25.049  54.314  1.00 89.38      AAAA C
ATOM  2491  CD  GLU  259      58.364  25.032  55.057  1.00 97.77      AAAA C
ATOM  2492  OE1 GLU  259      58.080  24.088  55.838  1.00101.45      AAAA O
ATOM  2493  OE2 GLU  259      57.598  26.002  54.837  1.00 94.58      AAAA O
ATOM  2494  C   GLU  259      62.117  28.078  54.083  1.00 85.43      AAAA C
ATOM  2495  O   GLU  259      62.059  29.009  54.903  1.00 88.01      AAAA O
ATOM  2496  N   SER  260      62.298  28.538  52.799  1.00 84.66      AAAA N
ATOM  2498  CA  SER  260      62.725  29.625  52.254  1.00 84.03      AAAA C
ATOM  2499  CB  SER  260      63.753  29.269  51.173  1.00 87.24      AAAA C
ATOM  2500  OG  SER  260      63.306  29.419  49.835  1.00 93.65      AAAA O
ATOM  2502  C   SER  260      61.558  30.466  51.789  1.00 80.84      AAAA C
ATOM  2503  O   SER  260      61.496  30.889  50.635  1.00 81.31      AAAA O
ATOM  2504  N   SER  261      60.617  30.785  52.685  1.00 78.56      AAAA N
ATOM  2506  CA  SER  261      59.423  31.540  52.308  1.00 72.13      AAAA C
ATOM  2507  CB  SER  261      58.179  31.297  53.170  1.00 67.30      AAAA C
ATOM  2508  OG  SER  261      57.436  30.334  52.451  1.00 74.74      AAAA O
ATOM  2510  C   SER  261      59.683  33.032  52.318  1.00 66.90      AAAA C
ATOM  2511  O   SER  261      60.048  33.588  53.334  1.00 63.24      AAAA O
ATOM  2512  N   ASP  262      59.364  33.659  51.204  1.00 65.30      AAAA N
ATOM  2514  CA  ASP  262      59.358  35.071  50.915  1.00 58.55      AAAA C
ATOM  2515  CB  ASP  262      59.268  35.285  49.400  1.00 64.85      AAAA C
ATOM  2516  CG  ASP  262      59.389  36.713  48.931  1.00 76.42      AAAA C
ATOM  2517  OD1 ASP  262      59.473  37.708  49.701  1.00 79.81      AAAA O
ATOM  2518  OD2 ASP  262      59.404  36.873  47.671  1.00 80.46      AAAA O
ATOM  2519  C   ASP  262      58.121  35.706  51.529  1.00 56.88      AAAA C
ATOM  2520  O   ASP  262      57.851  36.918  51.519  1.00 52.48      AAAA O
ATOM  2521  N   SER  263      57.259  34.849  52.119  1.00 53.43      AAAA N
ATOM  2523  CA  SER  263      56.047  35.352  52.734  1.00 52.84      AAAA C
ATOM  2524  CB  SER  263      55.020  34.245  52.985  1.00 46.60      AAAA C
ATOM  2525  OG  SER  263      55.149  33.348  51.791  1.00 66.80      AAAA O
ATOM  2527  C   SER  263      56.310  35.965  54.117  1.00 49.52      AAAA C
ATOM  2528  O   SER  263      57.396  35.737  54.709  1.00 42.33      AAAA O
ATOM  2529  N   GLU  264      55.320  36.783  54.540  1.00 38.93      AAAA N
ATOM  2531  CA  GLU  264      55.362  37.222  55.921  1.00 36.70      AAAA C
ATOM  2532  CB  GLU  264      54.359  38.337  56.208  1.00 43.71      AAAA C
ATOM  2533  CG  GLU  264      54.575  39.482  55.218  1.00 37.74      AAAA C
ATOM  2534  CD  GLU  264      55.374  40.632  55.793  1.00 34.36      AAAA C
ATOM  2535  OE1 GLU  264      55.493  40.600  57.034  1.00 41.55      AAAA O
ATOM  2536  OE2 GLU  264      55.832  41.576  55.146  1.00 39.60      AAAA O
ATOM  2537  C   GLU  264      55.098  36.056  56.827  1.00 35.84      AAAA C
ATOM  2538  O   GLU  264      54.368  35.151  56.355  1.00 39.60      AAAA O
ATOM  2539  N   GLY  265      55.801  35.938  57.962  1.00 35.64      AAAA N
ATOM  2541  CA  GLY  265      55.671  34.690  58.727  1.00 40.30      AAAA C
ATOM  2542  C   GLY  265      54.622  34.716  59.829  1.00 39.51      AAAA C
ATOM  2543  O   GLY  265      53.951  35.699  60.135  1.00 37.20      AAAA O
ATOM  2544  N   PHE  266      54.537  33.569  60.516  1.00 35.75      AAAA N
ATOM  2546  CA  PHE  266      53.637  33.434  61.625  1.00 33.70      AAAA C
ATOM  2547  CB  PHE  266      53.924  32.155  62.396  1.00 28.20      AAAA C
ATOM  2548  CG  PHE  266      53.356  30.958  61.671  1.00 37.07      AAAA C
ATOM  2549  CD1 PHE  266      53.760  30.618  60.377  1.00 34.72      AAAA C
ATOM  2550  CD2 PHE  266      52.383  30.185  62.313  1.00 25.65      AAAA C
ATOM  2551  CE1 PHE  266      53.225  29.506  59.760  1.00 37.72      AAAA C
ATOM  2552  CE2 PHE  266      51.879  29.094  61.672  1.00 24.63      AAAA C
ATOM  2553  CZ  PHE  266      52.260  28.708  60.402  1.00 23.58      AAAA C
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ATOM  2555  O   PHE  266      54.446  35.372  62.879  1.00 39.23      AAAA O
ATOM  2556  N   VAL  267      52.360  34.763  63.161  1.00 37.10      AAAA N
ATOM  2558  CA  VAL  267      52.118  35.812  64.113  1.00 36.09      AAAA C
ATOM  2559  CB  VAL  267      51.315  36.974  63.567  1.00 39.01      AAAA C
ATOM  2560  CG1 VAL  267      51.626  37.601  62.230  1.00 31.10      AAAA C
ATOM  2561  CG2 VAL  267      49.990  36.400  63.570  1.00 36.88      AAAA C
ATOM  2562  C   VAL  267      51.506  35.260  65.400  1.00 33.55      AAAA C
ATOM  2563  O   VAL  267      51.202  34.098  65.515  1.00 32.41      AAAA O
ATOM  2564  N   ILE  268      51.539  36.088  66.477  1.00 35.98      AAAA N
ATOM  2566  CA  ILE  268      50.867  35.573  67.681  1.00 39.79      AAAA C
ATOM  2567  CB  ILE  268      51.791  35.232  68.849  1.00 31.17      AAAA C
ATOM  2568  CG2 ILE  268      50.922  35.253  70.150  1.00 32.66      AAAA C
ATOM  2569  CG1 ILE  268      52.403  33.866  68.724  1.00 23.56      AAAA C
ATOM  2570  CD1 ILE  268      53.421  33.546  69.806  1.00 25.93      AAAA C
ATOM  2571  C   ILE  268      49.806  36.608  68.060  1.00 42.44      AAAA C
ATOM  2572  O   ILE  268      50.116  37.767  68.327  1.00 39.99      AAAA O
ATOM  2573  N   HIS  269      48.528  36.292  67.864  1.00 44.26      AAAA N
ATOM  2575  CA  HIS  269      47.491  37.320  68.173  1.00 44.28      AAAA C
ATOM  2576  CB  HIS  269      46.885  37.876  66.901  1.00 45.48      AAAA C
ATOM  2577  CG  HIS  269      45.915  38.986  67.079  1.00 54.33      AAAA C
ATOM  2578  CD2 HIS  269      44.551  39.014  67.096  1.00 46.61      AAAA C
ATOM  2579  ND1 HIS  269      46.356  40.280  67.307  1.00 51.86      AAAA N
ATOM  2581  CE1 HIS  269      45.282  41.057  67.437  1.00 55.17      AAAA C
ATOM  2582  NE2 HIS  269      44.175  40.324  67.309  1.00 46.97      AAAA N
ATOM  2584  C   HIS  269      46.423  36.740  69.074  1.00 45.54      AAAA C
ATOM  2585  O   HIS  269      46.076  35.552  69.027  1.00 42.94      AAAA O
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ATOM	2588	CA	ASP	270	44.948	37.025	71.001	1.00	48.03	AAAA C
ATOM	2589	CB	ASP	270	43.573	37.014	70.338	1.00	63.63	AAAA C
ATOM	2590	CG	ASP	270	42.919	38.393	70.294	1.00	80.82	AAAA C
ATOM	2591	OD1	ASP	270	41.737	38.379	69.835	1.00	90.92	AAAA O
ATOM	2592	OD2	ASP	270	43.407	39.494	70.652	1.00	86.49	AAAA O
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ATOM	2594	O	ASP	270	44.357	34.782	71.576	1.00	45.54	AAAA O
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ATOM	2597	CA	GLY	271	46.839	34.117	72.506	1.00	37.20	AAAA C
ATOM	2598	C	GLY	271	46.818	32.998	71.537	1.00	39.15	AAAA C
ATOM	2599	O	GLY	271	46.775	31.865	72.039	1.00	46.56	AAAA O
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ATOM	2602	CA	GLU	272	47.108	32.092	69.371	1.00	43.56	AAAA C
ATOM	2603	CB	GLU	272	45.752	31.737	68.876	1.00	37.58	AAAA C
ATOM	2604	CG	GLU	272	45.778	30.600	67.839	1.00	45.30	AAAA C
ATOM	2605	CD	GLU	272	44.413	30.528	67.149	1.00	36.92	AAAA C
ATOM	2606	OE1	GLU	272	43.545	31.345	67.533	1.00	48.41	AAAA O
ATOM	2607	OE2	GLU	272	44.223	29.696	66.286	1.00	44.10	AAAA O
ATOM	2608	C	GLU	272	48.211	32.324	68.335	1.00	40.32	AAAA C
ATOM	2609	O	GLU	272	48.445	33.447	67.896	1.00	37.04	AAAA O
ATOM	2610	N	CYS	273	48.942	31.237	68.138	1.00	38.83	AAAA N
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ATOM	2613	C	CYS	273	49.321	30.810	65.883	1.00	42.16	AAAA C
ATOM	2614	O	CYS	273	48.713	29.712	65.831	1.00	40.86	AAAA O
ATOM	2615	CB	CYS	273	51.098	30.148	67.529	1.00	40.21	AAAA C
ATOM	2616	SG	CYS	273	52.337	29.825	66.260	1.00	39.79	AAAA S
ATOM	2617	N	MET	274	49.373	31.749	64.933	1.00	33.70	AAAA N
ATOM	2619	CA	MET	274	48.586	31.351	63.720	1.00	36.68	AAAA C
ATOM	2620	CB	MET	274	47.136	31.861	63.847	1.00	29.11	AAAA C
ATOM	2621	CG	MET	274	46.923	33.379	63.691	1.00	36.51	AAAA C
ATOM	2622	SD	MET	274	45.477	33.921	64.677	1.00	40.00	AAAA S
ATOM	2623	CE	MET	274	45.659	35.658	64.754	1.00	22.47	AAAA C
ATOM	2624	C	MET	274	49.426	31.900	62.608	1.00	39.35	AAAA C
ATOM	2625	O	MET	274	50.167	32.880	62.672	1.00	41.00	AAAA O
ATOM	2626	N	GLN	275	49.378	31.353	61.428	1.00	42.55	AAAA N
ATOM	2628	CA	GLN	275	50.041	31.834	60.232	1.00	37.69	AAAA C
ATOM	2629	CB	GLN	275	49.618	30.765	59.242	1.00	34.01	AAAA C
ATOM	2630	CG	GLN	275	49.329	31.274	57.864	1.00	56.40	AAAA C
ATOM	2631	CD	GLN	275	49.275	30.190	56.812	1.00	66.46	AAAA C
ATOM	2632	OE1	GLN	275	49.941	29.151	56.910	1.00	67.24	AAAA O
ATOM	2633	NE2	GLN	275	48.451	30.436	55.799	1.00	78.29	AAAA N
ATOM	2636	C	GLN	275	49.721	33.195	59.720	1.00	35.41	AAAA C
ATOM	2637	O	GLN	275	50.526	33.831	59.064	1.00	35.95	AAAA O
ATOM	2638	N	GLU	276	48.566	33.754	60.056	1.00	41.70	AAAA N
ATOM	2640	CA	GLU	276	48.222	35.080	59.571	1.00	43.96	AAAA C
ATOM	2641	CB	GLU	276	47.387	34.884	58.245	1.00	42.40	AAAA C
ATOM	2642	CG	GLU	276	47.154	36.269	57.650	1.00	53.84	AAAA C
ATOM	2643	CD	GLU	276	48.359	37.198	57.460	1.00	61.37	AAAA C
ATOM	2644	OE1	GLU	276	49.356	36.595	56.943	1.00	67.32	AAAA O
ATOM	2645	OE2	GLU	276	48.242	38.411	57.811	1.00	45.10	AAAA O
ATOM	2646	C	GLU	276	47.444	35.935	60.540	1.00	39.74	AAAA C
ATOM	2647	O	GLU	276	46.760	35.449	61.444	1.00	45.06	AAAA O
ATOM	2648	N	CYS	277	47.495	37.235	60.500	1.00	38.69	AAAA N
ATOM	2650	CA	CYS	277	46.718	38.089	61.332	1.00	46.11	AAAA C
ATOM	2651	C	CYS	277	45.205	37.938	60.994	1.00	52.70	AAAA C
ATOM	2652	O	CYS	277	44.760	37.511	59.936	1.00	49.43	AAAA O
ATOM	2653	CB	CYS	277	47.039	39.537	61.111	1.00	45.56	AAAA C
ATOM	2654	SG	CYS	277	48.629	40.083	61.645	1.00	52.86	AAAA S
ATOM	2655	N	PRO	278	44.380	38.261	61.993	1.00	54.63	AAAA N
ATOM	2656	CD	PRO	278	44.824	38.778	63.311	1.00	57.20	AAAA C
ATOM	2657	CA	PRO	278	42.946	38.185	61.899	1.00	55.82	AAAA C
ATOM	2658	CB	PRO	278	42.445	38.635	63.267	1.00	55.61	AAAA C
ATOM	2659	CG	PRO	278	43.605	38.670	64.153	1.00	55.58	AAAA C
ATOM	2660	C	PRO	278	42.487	39.116	60.781	1.00	52.55	AAAA C
ATOM	2661	O	PRO	278	43.083	40.195	60.631	1.00	48.76	AAAA O
ATOM	2662	N	SER	279	41.370	38.845	60.143	1.00	49.35	AAAA N
ATOM	2664	CA	SER	279	40.915	39.720	59.140	1.00	52.03	AAAA C
ATOM	2665	CB	SER	279	39.280	39.572	58.975	1.00	47.62	AAAA C
ATOM	2666	OG	SER	279	39.320	38.778	57.785	1.00	68.16	AAAA O
ATOM	2668	C	SER	279	41.003	41.209	59.173	1.00	55.40	AAAA C
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ATOM	2670	N	GLY	280	40.775	41.962	60.247	1.00	55.32	AAAA N
ATOM	2672	CA	GLY	280	40.968	43.406	59.868	1.00	48.58	AAAA C
ATOM	2673	C	GLY	280	42.248	43.890	60.479	1.00	55.98	AAAA C
ATOM	2674	O	GLY	280	42.249	45.097	60.772	1.00	56.00	AAAA O
ATOM	2675	N	PHE	281	43.213	42.983	60.742	1.00	55.42	AAAA N
ATOM	2677	CA	PHE	281	44.506	43.411	61.262	1.00	52.94	AAAA C
ATOM	2678	CB	PHE	281	44.938	42.644	62.523	1.00	61.20	AAAA C
ATOM	2679	CG	PHE	281	43.958	42.792	63.637	1.00	53.66	AAAA C
ATOM	2680	CD1	PHE	281	44.142	43.702	64.630	1.00	60.47	AAAA C
ATOM	2681	CD2	PHE	281	42.939	41.992	63.712	1.00	60.99	AAAA C
ATOM	2682	CE1	PHE	281	43.272	43.901	65.678	1.00	64.71	AAAA C
ATOM	2683	CE2	PHE	281	41.931	42.162	64.756	1.00	63.19	AAAA C
ATOM	2684	CZ	PHE	281	42.141	43.115	65.744	1.00	58.88	AAAA C

ATOM	2685	C	PHE	281	45.630	43.217	60.240	1.00	48.00	AAAA C
ATOM	2686	O	PHE	281	45.738	42.395	59.327	1.00	38.84	AAAA O
ATOM	2687	N	ILE	282	46.670	43.990	60.557	1.00	49.55	AAAA N
ATOM	2689	CA	ILE	282	47.907	43.984	59.748	1.00	45.00	AAAA C
ATOM	2690	CB	ILE	282	47.945	45.188	58.799	1.00	30.25	AAAA C
ATOM	2691	CG2	ILE	282	48.041	46.494	59.507	1.00	24.60	AAAA C
ATOM	2692	CG1	ILE	282	49.092	45.022	57.795	1.00	38.71	AAAA C
ATOM	2693	CD1	ILE	282	49.194	46.043	56.669	1.00	33.38	AAAA C
ATOM	2694	C	ILE	282	49.081	43.889	60.673	1.00	44.30	AAAA C
ATOM	2695	O	ILE	282	49.078	44.447	61.759	1.00	48.49	AAAA O
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ATOM	2699	CB	ARG	283	52.300	42.200	60.286	1.00	41.10	AAAA C
ATOM	2700	CG	ARG	283	52.295	40.696	60.515	1.00	29.19	AAAA C
ATOM	2701	CD	ARG	283	53.078	39.986	59.451	1.00	29.85	AAAA C
ATOM	2702	NE	ARG	283	52.823	38.545	59.404	1.00	29.39	AAAA N
ATOM	2704	CZ	ARG	283	51.862	38.024	58.646	1.00	37.61	AAAA C
ATOM	2705	NH1	ARG	283	51.065	38.846	57.944	1.00	31.41	AAAA N
ATOM	2708	NH2	ARG	283	51.651	36.722	58.596	1.00	31.97	AAAA N
ATOM	2711	C	ARG	283	51.945	44.498	61.190	1.00	42.27	AAAA C
ATOM	2712	O	ARG	283	51.931	45.228	60.173	1.00	43.42	AAAA O
ATOM	2713	N	ASN	284	52.362	44.886	62.422	1.00	39.49	AAAA N
ATOM	2715	CA	ASN	284	52.733	46.311	62.574	1.00	42.07	AAAA C
ATOM	2721	C	ASN	284	54.078	46.656	61.929	1.00	41.64	AAAA C
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ATOM	2716	CB	ASN	284	52.734	46.760	64.032	1.00	37.33	AAAA C
ATOM	2717	CG	ASN	284	53.917	46.028	64.611	1.00	50.21	AAAA C
ATOM	2718	OD1	ASN	284	54.609	45.104	64.192	1.00	44.30	AAAA O
ATOM	2719	ND2	ASN	284	54.323	46.432	65.842	1.00	42.46	AAAA N
ATOM	2723	N	GLY	285	54.931	45.699	61.562	1.00	40.10	AAAA N
ATOM	2725	CA	GLY	285	55.971	45.815	60.593	1.00	26.91	AAAA C
ATOM	2726	C	GLY	285	56.091	44.468	59.848	1.00	33.12	AAAA C
ATOM	2727	O	GLY	285	55.584	43.331	60.187	1.00	29.51	AAAA O
ATOM	2728	N	SER	286	56.915	44.619	58.766	1.00	26.53	AAAA N
ATOM	2730	CA	SER	286	57.109	43.385	57.975	1.00	32.67	AAAA C
ATOM	2731	CB	SER	286	57.944	43.681	56.757	1.00	33.19	AAAA C
ATOM	2732	OG	SER	286	58.283	42.480	56.014	1.00	31.95	AAAA O
ATOM	2734	C	SER	286	57.750	42.310	58.836	1.00	34.57	AAAA C
ATOM	2735	O	SER	286	58.700	42.495	59.607	1.00	44.29	AAAA O
ATOM	2736	N	GLN	287	57.227	41.148	58.940	1.00	34.45	AAAA N
ATOM	2738	CA	GLN	287	57.738	40.005	59.634	1.00	35.25	AAAA C
ATOM	2739	CB	GLN	287	59.139	39.610	59.083	1.00	27.97	AAAA C
ATOM	2740	CG	GLN	287	59.037	39.234	57.664	1.00	26.61	AAAA C
ATOM	2741	CD	GLN	287	58.539	37.963	57.130	1.00	21.25	AAAA C
ATOM	2742	OE1	GLN	287	58.192	37.023	57.845	1.00	28.18	AAAA O
ATOM	2743	NE2	GLN	287	58.492	37.838	55.782	1.00	27.55	AAAA N
ATOM	2746	C	GLN	287	57.773	40.286	61.111	1.00	30.25	AAAA C
ATOM	2747	O	GLN	287	58.163	39.415	61.908	1.00	32.78	AAAA O
ATOM	2748	N	SER	288	57.021	41.217	61.624	1.00	32.49	AAAA N
ATOM	2750	CA	SER	288	56.696	41.322	63.043	1.00	28.98	AAAA C
ATOM	2751	CB	SER	288	56.024	42.675	63.313	1.00	35.79	AAAA C
ATOM	2752	OG	SER	288	55.639	42.612	64.701	1.00	36.61	AAAA O
ATOM	2754	C	SER	288	55.665	40.285	63.442	1.00	28.96	AAAA C
ATOM	2755	O	SER	288	54.993	39.776	62.553	1.00	31.16	AAAA O
ATOM	2756	N	MET	289	55.774	39.720	64.621	1.00	32.51	AAAA N
ATOM	2758	CA	MET	289	54.875	38.697	65.105	1.00	34.53	AAAA C
ATOM	2759	CB	MET	289	55.507	37.823	66.153	1.00	30.31	AAAA C
ATOM	2760	CG	MET	289	56.571	36.872	65.680	1.00	40.50	AAAA C
ATOM	2761	SD	MET	289	56.977	35.623	66.881	1.00	31.65	AAAA S
ATOM	2762	CE	MET	289	55.745	34.315	66.508	1.00	30.47	AAAA C
ATOM	2763	C	MET	289	53.557	39.286	65.703	1.00	35.55	AAAA C
ATOM	2764	O	MET	289	52.630	38.512	66.014	1.00	38.37	AAAA O
ATOM	2765	N	TYR	290	53.380	40.565	65.742	1.00	29.54	AAAA N
ATOM	2767	CA	TYR	290	52.363	41.358	66.297	1.00	38.81	AAAA C
ATOM	2768	CB	TYR	290	52.947	42.589	67.042	1.00	36.72	AAAA C
ATOM	2769	CG	TYR	290	53.570	42.184	68.351	1.00	41.94	AAAA C
ATOM	2770	CD1	TYR	290	54.932	41.780	68.350	1.00	37.79	AAAA C
ATOM	2771	CE1	TYR	290	55.548	41.368	69.503	1.00	32.60	AAAA C
ATOM	2772	CD2	TYR	290	52.987	42.157	69.570	1.00	39.93	AAAA C
ATOM	2773	CE2	TYR	290	53.501	41.750	70.748	1.00	36.16	AAAA C
ATOM	2774	CZ	TYR	290	54.822	41.355	70.693	1.00	38.85	AAAA C
ATOM	2775	OH	TYR	290	55.581	40.923	71.751	1.00	43.41	AAAA O
ATOM	2777	C	TYR	290	51.361	41.955	65.270	1.00	45.54	AAAA C
ATOM	2778	O	TYR	290	51.733	42.520	64.227	1.00	47.10	AAAA O
ATOM	2779	N	CYS	291	50.071	41.698	65.537	1.00	44.68	AAAA N
ATOM	2781	CA	CYS	291	49.017	42.205	64.685	1.00	47.20	AAAA C
ATOM	2782	C	CYS	291	48.285	43.434	65.194	1.00	46.06	AAAA C
ATOM	2783	O	CYS	291	47.892	43.550	66.343	1.00	49.45	AAAA O
ATOM	2784	CB	CYS	291	47.973	41.103	64.483	1.00	43.44	AAAA C
ATOM	2785	SG	CYS	291	48.766	39.715	63.683	1.00	45.49	AAAA S
ATOM	2786	N	ILE	292	48.136	44.453	64.365	1.00	46.82	AAAA N
ATOM	2788	CA	ILE	292	47.399	45.651	64.755	1.00	50.64	AAAA C
ATOM	2789	CB	ILE	292	48.267	46.932	64.779	1.00	39.19	AAAA C
ATOM	2790	CG2	ILE	292	49.291	46.885	65.861	1.00	44.39	AAAA C
ATOM	2791	CG1	ILE	292	48.920	47.095	63.402	1.00	44.25	AAAA C

ATOM	2792	CD1	ILE	292	49.234	48.568	63.109	1.00	32.80	AAAA C
ATOM	2793	C	ILE	292	46.240	46.003	63.806	1.00	50.01	AAAA C
ATOM	2794	O	ILE	292	46.165	45.526	62.670	1.00	46.64	AAAA O
ATOM	2795	N	PRO	293	45.150	46.507	64.385	1.00	51.86	AAAA N
ATOM	2796	CD	PRO	293	45.009	46.804	65.839	1.00	51.05	AAAA C
ATOM	2797	CA	PRO	293	43.958	46.930	63.675	1.00	51.40	AAAA C
ATOM	2798	CB	PRO	293	43.170	47.784	64.681	1.00	49.00	AAAA C
ATOM	2799	CG	PRO	293	43.533	47.112	65.951	1.00	53.73	AAAA C
ATOM	2800	C	PRO	293	44.253	47.870	62.525	1.00	51.68	AAAA C
ATOM	2801	O	PRO	293	45.053	48.788	62.737	1.00	51.92	AAAA O
ATOM	2802	N	CYS	294	43.607	47.621	61.408	1.00	50.66	AAAA N
ATOM	2804	CA	CYS	294	43.811	48.464	60.254	1.00	57.90	AAAA C
ATOM	2805	C	CYS	294	43.219	49.848	60.345	1.00	59.59	AAAA C
ATOM	2806	O	CYS	294	43.744	50.814	59.785	1.00	60.87	AAAA O
ATOM	2807	CB	CYS	294	43.229	47.686	59.046	1.00	57.59	AAAA C
ATOM	2808	SG	CYS	294	44.408	46.460	58.563	1.00	51.12	AAAA S
ATOM	2809	N	ALA	295	42.009	50.031	60.854	1.00	65.87	AAAA N
ATOM	2811	CA	ALA	295	41.391	51.386	60.804	1.00	71.19	AAAA C
ATOM	2812	CB	ALA	295	42.311	52.459	61.393	1.00	63.82	AAAA C
ATOM	2813	C	ALA	295	40.971	51.770	59.370	1.00	69.17	AAAA C
ATOM	2814	O	ALA	295	41.421	52.717	58.762	1.00	64.70	AAAA O
ATOM	2815	N	GLY	296	40.153	50.920	58.775	1.00	71.30	AAAA N
ATOM	2817	CA	GLY	296	39.640	51.049	57.416	1.00	72.66	AAAA C
ATOM	2818	C	GLY	296	39.895	49.686	56.769	1.00	74.20	AAAA C
ATOM	2819	O	GLY	296	40.408	48.819	57.490	1.00	75.04	AAAA O
ATOM	2820	N	PRO	297	39.561	49.540	55.497	1.00	71.98	AAAA N
ATOM	2821	CD	PRO	297	38.928	50.561	54.637	1.00	72.15	AAAA C
ATOM	2822	CA	PRO	297	39.958	48.344	54.777	1.00	68.23	AAAA C
ATOM	2823	CB	PRO	297	39.488	48.603	53.369	1.00	72.57	AAAA C
ATOM	2824	CG	PRO	297	38.470	49.687	53.490	1.00	74.04	AAAA C
ATOM	2825	C	PRO	297	41.480	48.306	54.860	1.00	65.78	AAAA C
ATOM	2826	O	PRO	297	42.147	49.323	54.997	1.00	62.72	AAAA O
ATOM	2827	N	CYS	298	42.039	47.135	55.073	1.00	63.85	AAAA N
ATOM	2829	CA	CYS	298	43.464	46.953	55.248	1.00	54.47	AAAA C
ATOM	2830	C	CYS	298	44.109	47.303	53.908	1.00	54.56	AAAA C
ATOM	2831	O	CYS	298	43.621	47.030	52.820	1.00	54.83	AAAA O
ATOM	2832	CB	CYS	298	43.665	45.544	55.669	1.00	47.65	AAAA C
ATOM	2833	SG	CYS	298	43.501	45.115	57.371	1.00	46.12	AAAA S
ATOM	2834	N	PRO	299	45.310	47.876	53.967	1.00	49.83	AAAA N
ATOM	2835	CD	PRO	299	46.087	48.168	55.194	1.00	48.14	AAAA C
ATOM	2836	CA	PRO	299	46.055	48.212	52.787	1.00	43.67	AAAA C
ATOM	2837	CB	PRO	299	47.267	48.965	53.281	1.00	44.08	AAAA C
ATOM	2838	CG	PRO	299	47.454	48.361	54.628	1.00	51.38	AAAA C
ATOM	2839	C	PRO	299	46.341	46.969	52.010	1.00	38.86	AAAA C
ATOM	2840	O	PRO	299	46.372	45.874	52.546	1.00	42.85	AAAA O
ATOM	2841	N	LYS	300	46.310	47.073	50.712	1.00	38.30	AAAA N
ATOM	2843	CA	LYS	300	46.484	45.958	49.812	1.00	42.62	AAAA C
ATOM	2844	CB	LYS	300	45.176	45.226	49.595	1.00	34.28	AAAA C
ATOM	2845	CG	LYS	300	45.346	43.901	48.920	1.00	41.45	AAAA C
ATOM	2846	CD	LYS	300	44.013	43.413	48.378	1.00	48.31	AAAA C
ATOM	2847	CE	LYS	300	44.388	42.027	47.787	1.00	48.57	AAAA C
ATOM	2848	NZ	LYS	300	43.662	42.031	46.478	1.00	63.70	AAAA N
ATOM	2852	C	LYS	300	46.964	46.479	48.432	1.00	48.72	AAAA C
ATOM	2853	O	LYS	300	46.413	47.383	47.776	1.00	46.09	AAAA O
ATOM	2854	N	VAL	301	48.150	45.984	48.054	1.00	48.15	AAAA N
ATOM	2856	CA	VAL	301	48.802	46.462	46.871	1.00	44.52	AAAA C
ATOM	2857	CB	VAL	301	50.292	46.729	47.074	1.00	51.52	AAAA C
ATOM	2858	CG1	VAL	301	51.008	47.200	45.796	1.00	43.07	AAAA C
ATOM	2859	CG2	VAL	301	50.495	47.794	48.141	1.00	49.50	AAAA C
ATOM	2860	C	VAL	301	48.526	45.410	45.837	1.00	44.59	AAAA C
ATOM	2861	O	VAL	301	48.913	44.291	46.060	1.00	43.70	AAAA O
ATOM	2862	N	CYS	302	47.910	45.816	44.718	1.00	47.98	AAAA N
ATOM	2864	CA	CYS	302	47.645	44.735	43.739	1.00	55.19	AAAA C
ATOM	2865	C	CYS	302	48.594	44.968	42.583	1.00	57.64	AAAA C
ATOM	2866	O	CYS	302	48.852	46.152	42.313	1.00	60.23	AAAA O
ATOM	2867	CB	CYS	302	46.186	44.630	43.330	1.00	68.30	AAAA C
ATOM	2868	SG	CYS	302	45.070	44.360	44.751	1.00	70.31	AAAA S
ATOM	2869	N	GLU	303	49.183	43.921	42.075	1.00	58.15	AAAA N
ATOM	2871	CA	GLU	303	50.174	43.932	41.034	1.00	62.85	AAAA C
ATOM	2872	CB	GLU	303	51.603	44.006	41.595	1.00	67.85	AAAA C
ATOM	2873	CG	GLU	303	51.760	43.487	43.014	0.01	67.46	AAAA C
ATOM	2874	CD	GLU	303	51.999	41.992	43.097	0.01	67.94	AAAA C
ATOM	2875	OE1	GLU	303	53.011	41.514	42.561	0.01	67.67	AAAA O
ATOM	2876	OE2	GLU	303	51.147	41.290	43.697	0.01	67.65	AAAA O
ATOM	2877	C	GLU	303	50.096	42.662	40.194	1.00	64.12	AAAA C
ATOM	2878	O	GLU	303	50.162	41.562	40.708	1.00	65.08	AAAA O
ATOM	2879	N	GLU	304	49.867	42.794	38.904	1.00	67.37	AAAA N
ATOM	2881	CA	GLU	304	49.672	41.583	38.094	1.00	74.63	AAAA C
ATOM	2882	CB	GLU	304	48.285	41.596	37.458	1.00	71.71	AAAA C
ATOM	2883	CG	GLU	304	47.339	42.663	38.031	1.00	84.54	AAAA C
ATOM	2884	CD	GLU	304	45.930	42.152	36.185	1.00	87.56	AAAA C
ATOM	2885	OE1	GLU	304	45.438	41.571	37.179	1.00	89.13	AAAA O
ATOM	2886	OE2	GLU	304	45.249	42.269	39.233	1.00	93.19	AAAA O
ATOM	2887	C	GLU	304	50.866	41.307	37.190	1.00	76.10	AAAA C
ATOM	2888	O	GLU	304	51.911	41.962	37.217	1.00	74.78	AAAA O

ATOM	2989	N	GLU	305	50.899	40.126	36.566	1.00	77.31	AAAA N
ATOM	2991	CA	GLU	305	51.932	39.656	35.674	1.00	75.90	AAAA C
ATOM	2992	CB	GLU	305	51.467	38.380	34.979	1.00	79.95	AAAA C
ATOM	2993	CG	GLU	305	52.307	37.937	33.807	1.00	87.29	AAAA C
ATOM	2994	CD	GLU	305	51.758	36.891	32.886	0.01	83.39	AAAA C
ATOM	2995	OE1	GLU	305	50.762	36.234	33.252	0.01	83.66	AAAA O
ATOM	2996	OE2	GLU	305	52.310	36.700	31.789	0.01	83.73	AAAA O
ATOM	2997	C	GLU	305	52.276	40.737	34.666	1.00	75.97	AAAA C
ATOM	2998	O	GLU	305	53.381	41.268	34.613	1.00	76.54	AAAA O
ATOM	2999	N	LYS	306	51.291	41.181	33.888	1.00	78.22	AAAA N
ATOM	3001	CA	LYS	306	51.479	42.329	33.004	1.00	75.99	AAAA C
ATOM	3002	CB	LYS	306	50.467	42.253	31.855	1.00	79.78	AAAA C
ATOM	3003	CG	LYS	306	51.208	42.227	30.527	1.00	94.52	AAAA C
ATOM	3004	CD	LYS	306	50.313	42.191	29.314	1.00	92.78	AAAA C
ATOM	3005	CE	LYS	306	50.740	43.227	28.261	1.00	97.10	AAAA C
ATOM	3006	NZ	LYS	306	50.938	44.554	28.929	1.00	84.87	AAAA N
ATOM	3010	C	LYS	306	51.381	43.669	33.703	1.00	73.85	AAAA C
ATOM	3011	O	LYS	306	50.703	43.862	34.718	1.00	76.08	AAAA O
ATOM	3012	N	LYS	307	52.000	44.700	33.180	1.00	71.15	AAAA N
ATOM	3014	CA	LYS	307	51.934	46.053	33.692	1.00	69.45	AAAA C
ATOM	3015	CB	LYS	307	53.022	46.903	33.008	1.00	79.64	AAAA C
ATOM	3016	CG	LYS	307	54.419	46.837	33.564	1.00	78.88	AAAA C
ATOM	3017	CD	LYS	307	55.257	48.084	33.374	1.00	85.84	AAAA C
ATOM	3018	CE	LYS	307	55.708	48.215	31.924	1.00	97.07	AAAA C
ATOM	3019	NZ	LYS	307	54.649	48.840	31.067	1.00	97.80	AAAA N
ATOM	3023	C	LYS	307	50.562	46.716	33.525	1.00	67.97	AAAA C
ATOM	3024	O	LYS	307	50.010	47.369	34.431	1.00	64.46	AAAA O
ATOM	3025	N	THR	308	49.979	46.661	32.323	1.00	65.84	AAAA N
ATOM	3027	CA	THR	308	48.709	47.319	32.091	1.00	64.56	AAAA C
ATOM	3028	CB	THR	308	48.714	47.977	30.711	1.00	59.91	AAAA C
ATOM	3029	OG1	THR	308	49.834	48.843	30.577	1.00	61.97	AAAA O
ATOM	3031	CG2	THR	308	47.392	48.742	30.561	1.00	63.64	AAAA C
ATOM	3032	C	THR	308	47.514	46.379	32.234	1.00	61.82	AAAA C
ATOM	3033	O	THR	308	47.412	45.415	31.477	1.00	62.05	AAAA O
ATOM	3034	N	LYS	309	46.675	46.719	33.211	1.00	55.66	AAAA N
ATOM	3036	CA	LYS	309	45.456	45.926	33.445	1.00	54.67	AAAA C
ATOM	3037	CB	LYS	309	45.043	45.880	34.904	1.00	56.82	AAAA C
ATOM	3038	CG	LYS	309	43.601	45.541	35.223	1.00	57.50	AAAA C
ATOM	3039	CD	LYS	309	43.390	44.039	35.086	1.00	59.50	AAAA C
ATOM	3040	CE	LYS	309	42.703	43.448	36.324	1.00	57.31	AAAA C
ATOM	3041	NZ	LYS	309	42.758	41.954	36.236	1.00	57.22	AAAA N
ATOM	3045	C	LYS	309	44.391	46.570	32.548	1.00	51.21	AAAA C
ATOM	3046	O	LYS	309	44.074	47.763	32.680	1.00	47.23	AAAA O
ATOM	3047	N	THR	310	43.895	45.772	31.610	1.00	47.67	AAAA N
ATOM	3049	CA	THR	310	42.862	46.328	30.733	1.00	51.89	AAAA C
ATOM	3050	CB	THR	310	43.161	46.015	29.266	1.00	54.81	AAAA C
ATOM	3051	OG1	THR	310	41.909	45.710	28.635	1.00	66.29	AAAA O
ATOM	3053	CG2	THR	310	44.032	44.791	29.139	1.00	55.18	AAAA C
ATOM	3054	C	THR	310	41.468	45.841	31.117	1.00	51.15	AAAA C
ATOM	3055	O	THR	310	41.162	44.680	30.991	1.00	49.27	AAAA O
ATOM	3056	N	ILE	311	40.684	46.706	31.732	1.00	50.18	AAAA N
ATOM	3058	CA	ILE	311	39.363	46.453	32.276	1.00	48.67	AAAA C
ATOM	3059	CB	ILE	311	39.120	47.396	33.462	1.00	49.27	AAAA C
ATOM	3060	CG2	ILE	311	37.655	47.596	33.799	1.00	50.72	AAAA C
ATOM	3061	CG1	ILE	311	39.896	46.930	34.699	1.00	41.34	AAAA C
ATOM	3062	CD1	ILE	311	39.847	48.073	35.739	1.00	52.22	AAAA C
ATOM	3063	C	ILE	311	38.334	46.729	31.186	1.00	45.37	AAAA C
ATOM	3064	O	ILE	311	38.132	47.875	30.758	1.00	37.14	AAAA O
ATOM	3065	N	ASP	312	37.871	45.678	30.524	1.00	50.10	AAAA N
ATOM	3067	CA	ASP	312	36.991	45.842	29.377	1.00	56.35	AAAA C
ATOM	3068	CB	ASP	312	37.546	45.152	28.128	1.00	59.45	AAAA C
ATOM	3069	CG	ASP	312	37.761	43.671	28.382	1.00	65.64	AAAA C
ATOM	3070	OD1	ASP	312	38.525	43.034	27.636	1.00	72.60	AAAA O
ATOM	3071	OD2	ASP	312	37.154	43.176	29.348	1.00	66.86	AAAA O
ATOM	3072	C	ASP	312	35.589	45.337	29.693	1.00	59.39	AAAA C
ATOM	3073	O	ASP	312	34.729	45.007	28.867	1.00	61.00	AAAA O
ATOM	3074	N	SER	313	35.278	45.290	30.976	1.00	61.17	AAAA N
ATOM	3076	CA	SER	313	34.053	44.683	31.459	1.00	55.73	AAAA C
ATOM	3077	CB	SER	313	34.121	43.201	31.093	1.00	48.22	AAAA C
ATOM	3078	OG	SER	313	34.373	42.514	32.292	1.00	57.89	AAAA O
ATOM	3080	C	SER	313	33.998	44.818	32.941	1.00	57.87	AAAA C
ATOM	3081	O	SER	313	34.802	45.506	33.537	1.00	66.47	AAAA O
ATOM	3082	N	VAL	314	33.001	44.205	33.545	1.00	64.35	AAAA N
ATOM	3084	CA	VAL	314	32.849	44.305	35.015	1.00	64.39	AAAA C
ATOM	3085	CB	VAL	314	31.360	44.340	35.343	1.00	69.57	AAAA C
ATOM	3086	CG1	VAL	314	31.024	43.693	36.681	1.00	65.60	AAAA C
ATOM	3087	CG2	VAL	314	30.927	45.823	35.319	1.00	65.27	AAAA C
ATOM	3088	C	VAL	314	33.492	43.088	35.638	1.00	62.65	AAAA C
ATOM	3089	O	VAL	314	34.029	43.141	36.704	1.00	63.92	AAAA O
ATOM	3090	N	THR	315	33.468	42.011	34.878	1.00	61.82	AAAA N
ATOM	3092	CA	THR	315	34.029	40.752	35.284	1.00	63.44	AAAA C
ATOM	3093	CB	THR	315	33.618	39.628	34.314	1.00	65.54	AAAA C
ATOM	3094	OG1	THR	315	32.403	40.004	33.634	1.00	74.05	AAAA O
ATOM	3096	CG2	THR	315	33.339	38.366	35.104	1.00	64.80	AAAA C
ATOM	3097	C	THR	315	35.541	40.871	35.323	1.00	65.62	AAAA C

ATOM	2998	O	THR	315	36.217	40.339	36.206	1.00	66.41	AAAA O
ATOM	2999	N	SER	316	36.071	41.593	34.332	1.00	63.28	AAAA N
ATOM	3001	CA	SER	316	37.500	41.793	34.215	1.00	58.72	AAAA C
ATOM	3002	CB	SER	316	37.785	42.537	32.900	1.00	52.20	AAAA C
ATOM	3003	OG	SER	316	37.298	43.859	32.933	1.00	48.04	AAAA O
ATOM	3005	C	SER	316	38.077	42.573	35.387	1.00	58.91	AAAA C
ATOM	3006	O	SER	316	39.293	42.522	35.520	1.00	59.86	AAAA O
ATOM	3007	N	ALA	317	37.310	43.362	36.111	1.00	55.86	AAAA N
ATOM	3009	CA	ALA	317	37.750	44.184	37.191	1.00	57.17	AAAA C
ATOM	3010	CB	ALA	317	36.833	45.409	37.269	1.00	54.23	AAAA C
ATOM	3011	C	ALA	317	37.689	43.487	38.538	1.00	62.05	AAAA C
ATOM	3012	O	ALA	317	37.702	44.128	39.599	1.00	60.30	AAAA O
ATOM	3013	N	GLN	318	37.361	42.205	38.523	1.00	67.91	AAAA N
ATOM	3015	CA	GLN	318	37.185	41.380	39.713	1.00	70.72	AAAA C
ATOM	3016	CB	GLN	318	36.857	39.956	39.293	1.00	74.48	AAAA C
ATOM	3017	CG	GLN	318	36.624	38.947	40.383	1.00	89.82	AAAA C
ATOM	3018	CD	GLN	318	35.265	39.080	41.048	1.00	92.69	AAAA C
ATOM	3019	OE1	GLN	318	34.256	38.807	40.391	1.00	98.57	AAAA O
ATOM	3020	NE2	GLN	318	35.356	39.509	42.308	1.00	92.51	AAAA N
ATOM	3023	C	GLN	318	38.380	41.413	40.653	1.00	72.63	AAAA C
ATOM	3024	O	GLN	318	38.294	41.855	41.804	1.00	68.92	AAAA O
ATOM	3025	N	MET	319	39.562	41.062	40.153	1.00	75.18	AAAA N
ATOM	3027	CA	MET	319	40.846	41.175	40.826	1.00	71.85	AAAA C
ATOM	3028	CB	MET	319	41.950	40.960	39.772	1.00	82.00	AAAA C
ATOM	3029	CG	MET	319	41.740	39.644	39.050	1.00	91.16	AAAA C
ATOM	3030	SD	MET	319	43.123	38.482	39.185	1.00	106.72	AAAA S
ATOM	3031	CE	MET	319	42.486	37.105	38.231	1.00	97.56	AAAA C
ATOM	3032	C	MET	319	41.118	42.509	41.471	1.00	67.68	AAAA C
ATOM	3033	O	MET	319	41.537	42.541	42.612	1.00	69.73	AAAA O
ATOM	3034	N	LEU	320	40.749	43.639	40.897	1.00	62.95	AAAA N
ATOM	3036	CA	LEU	320	40.907	44.938	41.531	1.00	62.31	AAAA C
ATOM	3037	CB	LEU	320	40.440	46.085	40.623	1.00	54.93	AAAA C
ATOM	3038	CG	LEU	320	41.091	46.163	39.238	1.00	53.48	AAAA C
ATOM	3039	CD1	LEU	320	41.005	47.552	38.692	1.00	51.31	AAAA C
ATOM	3040	CD2	LEU	320	42.557	45.709	39.403	1.00	58.43	AAAA C
ATOM	3041	C	LEU	320	40.209	45.008	42.881	1.00	60.30	AAAA C
ATOM	3042	O	LEU	320	40.344	45.969	43.661	1.00	58.72	AAAA O
ATOM	3043	N	GLN	321	39.267	44.106	43.112	1.00	59.62	AAAA N
ATOM	3045	CA	GLN	321	38.482	44.128	44.343	1.00	63.50	AAAA C
ATOM	3046	CB	GLN	321	37.373	43.089	44.250	1.00	62.52	AAAA C
ATOM	3047	CG	GLN	321	36.611	42.854	45.522	1.00	56.83	AAAA C
ATOM	3048	CD	GLN	321	35.337	42.064	45.291	1.00	68.77	AAAA C
ATOM	3049	OE1	GLN	321	35.362	40.969	44.718	1.00	70.37	AAAA O
ATOM	3050	NE2	GLN	321	34.218	42.632	45.764	1.00	63.77	AAAA N
ATOM	3053	C	GLN	321	39.367	44.030	45.594	1.00	60.97	AAAA C
ATOM	3054	O	GLN	321	40.262	43.196	45.782	1.00	57.29	AAAA O
ATOM	3055	N	GLY	322	39.092	44.928	46.546	1.00	57.62	AAAA N
ATOM	3057	CA	GLY	322	39.855	44.928	47.790	1.00	60.63	AAAA C
ATOM	3058	C	GLY	322	41.126	45.773	47.812	1.00	61.78	AAAA C
ATOM	3059	O	GLY	322	41.584	46.198	48.889	1.00	60.16	AAAA O
ATOM	3060	N	CYS	323	41.719	46.124	46.676	1.00	60.03	AAAA N
ATOM	3062	CA	CYS	323	42.938	46.845	46.528	1.00	54.20	AAAA C
ATOM	3063	C	CYS	323	42.924	48.307	46.910	1.00	53.48	AAAA C
ATOM	3064	O	CYS	323	42.105	49.148	46.503	1.00	56.43	AAAA O
ATOM	3065	CB	CYS	323	43.458	46.822	45.096	1.00	53.33	AAAA C
ATOM	3066	SG	CYS	323	43.325	45.222	44.248	1.00	66.22	AAAA S
ATOM	3067	N	THR	324	43.994	48.718	47.580	1.00	49.83	AAAA N
ATOM	3069	CA	THR	324	44.164	50.161	47.811	1.00	52.29	AAAA C
ATOM	3070	CB	THR	324	44.623	50.324	49.264	1.00	52.84	AAAA C
ATOM	3071	OG1	THR	324	45.245	49.087	49.634	1.00	59.82	AAAA O
ATOM	3073	CG2	THR	324	43.432	50.517	50.193	1.00	60.00	AAAA C
ATOM	3074	C	THR	324	45.154	50.802	46.844	1.00	48.91	AAAA C
ATOM	3075	O	THR	324	45.277	52.016	46.710	1.00	46.90	AAAA O
ATOM	3076	N	ILE	325	46.021	49.963	46.254	1.00	46.87	AAAA N
ATOM	3078	CA	ILE	325	47.114	50.511	45.445	1.00	45.10	AAAA C
ATOM	3079	CB	ILE	325	48.473	50.577	46.183	1.00	43.60	AAAA C
ATOM	3080	CG2	ILE	325	49.586	50.905	45.163	1.00	47.47	AAAA C
ATOM	3081	CG1	ILE	325	48.394	51.623	47.294	1.00	34.03	AAAA C
ATOM	3082	CD1	ILE	325	49.595	52.010	48.028	1.00	41.94	AAAA C
ATOM	3083	C	ILE	325	47.265	49.642	44.229	1.00	42.88	AAAA C
ATOM	3084	O	ILE	325	47.406	48.429	44.469	1.00	42.99	AAAA O
ATOM	3085	N	PHE	326	47.170	50.238	43.042	1.00	41.19	AAAA N
ATOM	3087	CA	PHE	326	47.312	49.334	41.880	1.00	42.98	AAAA C
ATOM	3088	CB	PHE	326	46.166	49.437	40.877	1.00	39.15	AAAA C
ATOM	3089	CG	PHE	326	46.403	48.474	39.738	1.00	38.03	AAAA C
ATOM	3090	CD1	PHE	326	46.186	47.125	39.951	1.00	39.68	AAAA C
ATOM	3091	CD2	PHE	326	46.917	48.892	38.525	1.00	37.31	AAAA C
ATOM	3092	CE1	PHE	326	46.447	46.139	39.023	1.00	36.52	AAAA C
ATOM	3093	CE2	PHE	326	47.136	47.919	37.551	1.00	45.74	AAAA C
ATOM	3094	CZ	PHE	326	46.924	46.570	37.787	1.00	39.92	AAAA C
ATOM	3095	C	PHE	326	48.682	49.673	41.280	1.00	48.78	AAAA C
ATOM	3096	O	PHE	326	49.024	50.826	40.966	1.00	51.39	AAAA O
ATOM	3097	N	LYS	327	49.623	48.751	41.379	1.00	50.22	AAAA N
ATOM	3099	CA	LYS	327	50.964	48.963	40.831	1.00	51.49	AAAA C
ATOM	3100	CB	LYS	327	52.050	48.091	41.519	1.00	58.64	AAAA C

ATOM	3101	CG	LYS	327	53.254	48.997	41.991	1.00	59.15	AAAA C
ATOM	3102	CD	LYS	327	54.528	48.257	41.617	1.00	63.49	AAAA C
ATOM	3103	CE	LYS	327	55.400	48.951	40.592	1.00	68.12	AAAA C
ATOM	3104	NZ	LYS	327	56.260	47.889	39.938	1.00	71.97	AAAA N
ATOM	3108	C	LYS	327	50.895	48.464	39.391	1.00	45.70	AAAA C
ATOM	3109	O	LYS	327	50.901	47.245	39.127	1.00	49.55	AAAA O
ATOM	3110	N	GLY	328	50.760	49.397	38.502	1.00	39.68	AAAA N
ATOM	3112	CA	GLY	328	50.647	49.038	37.080	1.00	39.44	AAAA C
ATOM	3113	C	GLY	328	49.845	50.161	36.427	1.00	39.49	AAAA C
ATOM	3114	O	GLY	328	49.858	51.307	36.881	1.00	31.92	AAAA O
ATOM	3115	N	ASN	329	49.286	49.813	35.289	1.00	41.47	AAAA N
ATOM	3117	CA	ASN	329	48.467	50.750	34.543	1.00	45.72	AAAA C
ATOM	3118	CB	ASN	329	49.185	50.942	33.211	1.00	42.50	AAAA C
ATOM	3119	CG	ASN	329	50.624	51.426	33.357	1.00	42.26	AAAA C
ATOM	3120	OD1	ASN	329	50.954	52.331	34.156	1.00	34.77	AAAA O
ATOM	3121	ND2	ASN	329	51.425	50.769	32.530	1.00	30.62	AAAA N
ATOM	3124	C	ASN	329	47.038	50.207	34.357	1.00	50.37	AAAA C
ATOM	3125	O	ASN	329	46.736	49.015	34.119	1.00	50.17	AAAA O
ATOM	3126	N	LEU	330	46.090	51.143	34.413	1.00	47.13	AAAA N
ATOM	3128	CA	LEU	330	44.691	50.860	34.151	1.00	42.53	AAAA C
ATOM	3129	CB	LEU	330	43.751	51.530	35.153	1.00	42.84	AAAA C
ATOM	3130	CG	LEU	330	43.768	50.995	36.598	1.00	38.65	AAAA C
ATOM	3131	CD1	LEU	330	42.864	51.924	37.417	1.00	38.12	AAAA C
ATOM	3132	CD2	LEU	330	43.283	49.565	36.669	1.00	38.74	AAAA C
ATOM	3133	C	LEU	330	44.352	51.377	32.758	1.00	39.10	AAAA C
ATOM	3134	O	LEU	330	44.509	52.545	32.460	1.00	40.71	AAAA O
ATOM	3135	N	LEU	331	43.933	50.516	31.904	1.00	36.10	AAAA N
ATOM	3137	CA	LEU	331	43.367	50.869	30.625	1.00	43.10	AAAA C
ATOM	3138	CB	LEU	331	43.958	49.894	29.585	1.00	42.29	AAAA C
ATOM	3139	CG	LEU	331	43.301	49.960	28.221	1.00	40.89	AAAA C
ATOM	3140	CD1	LEU	331	43.501	51.319	27.627	1.00	46.64	AAAA C
ATOM	3141	CD2	LEU	331	43.844	48.834	27.367	1.00	48.76	AAAA C
ATOM	3142	C	LEU	331	41.872	50.568	30.705	1.00	41.12	AAAA C
ATOM	3143	O	LEU	331	41.562	49.365	30.779	1.00	40.08	AAAA O
ATOM	3144	N	ILE	332	41.029	51.566	30.862	1.00	41.13	AAAA N
ATOM	3146	CA	ILE	332	39.606	51.241	31.044	1.00	36.90	AAAA C
ATOM	3147	CB	ILE	332	38.885	52.085	32.076	1.00	34.77	AAAA C
ATOM	3148	CG2	ILE	332	37.413	51.612	32.195	1.00	34.66	AAAA C
ATOM	3149	CG1	ILE	332	39.550	51.895	33.452	1.00	33.64	AAAA C
ATOM	3150	CD1	ILE	332	39.479	53.152	34.337	1.00	48.21	AAAA C
ATOM	3151	C	ILE	332	38.959	51.367	29.688	1.00	34.03	AAAA C
ATOM	3152	O	ILE	332	38.867	52.489	29.200	1.00	35.89	AAAA O
ATOM	3153	N	ASN	333	38.569	50.273	29.094	1.00	35.25	AAAA N
ATOM	3155	CA	ASN	333	38.014	50.283	27.737	1.00	40.34	AAAA C
ATOM	3156	CB	ASN	333	38.960	49.499	26.797	1.00	50.50	AAAA C
ATOM	3157	CG	ASN	333	38.668	49.493	25.310	1.00	59.29	AAAA C
ATOM	3158	OD1	ASN	333	37.845	48.711	24.784	1.00	64.54	AAAA O
ATOM	3159	ND2	ASN	333	39.290	50.350	24.467	1.00	45.83	AAAA N
ATOM	3162	C	ASN	333	36.666	49.581	27.755	1.00	47.63	AAAA C
ATOM	3163	O	ASN	333	36.462	48.409	27.398	1.00	44.40	AAAA O
ATOM	3164	N	ILE	334	35.644	50.213	28.315	1.00	54.13	AAAA N
ATOM	3166	CA	ILE	334	34.332	49.537	28.460	1.00	59.07	AAAA C
ATOM	3167	CB	ILE	334	33.788	49.826	29.876	1.00	61.98	AAAA C
ATOM	3168	CG2	ILE	334	32.362	49.355	30.047	1.00	54.04	AAAA C
ATOM	3169	CG1	ILE	334	34.737	49.224	30.915	1.00	60.43	AAAA C
ATOM	3170	CD1	ILE	334	34.346	49.687	32.317	1.00	68.57	AAAA C
ATOM	3171	C	ILE	334	33.271	50.032	27.476	1.00	59.45	AAAA C
ATOM	3172	O	ILE	334	32.726	51.136	27.635	1.00	56.22	AAAA O
ATOM	3173	N	ARG	335	32.919	49.181	26.550	1.00	59.69	AAAA N
ATOM	3175	CA	ARG	335	31.910	49.567	25.573	1.00	73.93	AAAA C
ATOM	3176	CB	ARG	335	32.262	48.903	24.240	1.00	74.44	AAAA C
ATOM	3177	CG	ARG	335	33.729	48.932	23.918	1.00	82.97	AAAA C
ATOM	3178	CD	ARG	335	34.102	49.289	22.500	1.00	86.49	AAAA C
ATOM	3179	NE	ARG	335	34.361	48.040	21.777	1.00	89.83	AAAA N
ATOM	3181	CZ	ARG	335	34.011	47.838	20.496	1.00	93.67	AAAA C
ATOM	3182	NH1	ARG	335	33.409	48.852	19.843	1.00	87.24	AAAA N
ATOM	3185	NH2	ARG	335	34.256	46.674	19.877	1.00	75.31	AAAA N
ATOM	3188	C	ARG	335	30.492	49.233	26.021	1.00	81.52	AAAA C
ATOM	3189	O	ARG	335	29.664	50.115	26.239	1.00	84.11	AAAA O
ATOM	3190	N	ALA	336	30.208	47.953	26.234	1.00	87.51	AAAA N
ATOM	3192	CA	ALA	336	28.878	47.484	26.601	1.00	92.40	AAAA C
ATOM	3193	CB	ALA	336	28.835	45.980	26.633	1.00	94.03	AAAA C
ATOM	3194	C	ALA	336	28.479	48.058	27.953	1.00	96.61	AAAA C
ATOM	3195	O	ALA	336	29.316	48.019	28.855	1.00	96.96	AAAA O
ATOM	3196	N	GLY	337	27.298	48.685	28.039	1.00	99.74	AAAA N
ATOM	3198	CA	GLY	337	26.986	49.385	29.272	1.00103.11		AAAA C
ATOM	3199	C	GLY	337	25.568	49.303	29.763	1.00105.51		AAAA C
ATOM	3200	O	GLY	337	24.801	50.267	29.596	1.00106.64		AAAA O
ATOM	3201	N	ASN	338	25.243	48.146	30.346	1.00105.41		AAAA N
ATOM	3203	CA	ASN	338	23.886	48.017	30.908	1.00106.92		AAAA C
ATOM	3204	CB	ASN	338	23.714	46.689	31.624	1.00109.14		AAAA C
ATOM	3205	CG	ASN	338	24.403	45.544	30.928	1.00112.30		AAAA C
ATOM	3206	OD1	ASN	338	25.598	45.595	30.625	1.00117.94		AAAA O
ATOM	3207	ND2	ASN	338	23.604	44.508	30.683	1.00113.72		AAAA N
ATOM	3210	C	ASN	338	23.790	49.160	31.931	1.00105.84		AAAA C

ATOM	3211	O	ASN	338	23.544	50.345	31.739	1.00103.97	AAAA O
ATOM	3212	N	ASN	339	24.290	48.762	33.099	1.00105.47	AAAA N
ATOM	3214	CA	ASN	339	24.529	49.740	34.159	1.00107.19	AAAA C
ATOM	3215	CB	ASN	339	23.252	49.915	34.945	1.00109.15	AAAA C
ATOM	3216	CG	ASN	339	22.777	51.351	35.003	0.01107.52	AAAA C
ATOM	3217	OD1	ASN	339	22.715	51.931	36.088	0.01107.49	AAAA O
ATOM	3218	ND2	ASN	339	22.441	51.932	33.859	0.01107.46	AAAA N
ATOM	3221	C	ASN	339	25.697	49.237	35.007	1.00106.33	AAAA C
ATOM	3222	O	ASN	339	25.520	48.390	35.886	1.00108.82	AAAA O
ATOM	3223	N	ILE	340	26.897	49.527	34.510	1.00101.36	AAAA N
ATOM	3225	CA	ILE	340	28.136	49.101	35.138	1.00 97.43	AAAA C
ATOM	3226	CB	ILE	340	29.040	48.354	34.151	1.00 93.63	AAAA C
ATOM	3227	CG2	ILE	340	28.194	47.252	33.489	1.00 99.38	AAAA C
ATOM	3228	CG1	ILE	340	29.726	49.158	33.070	1.00 85.50	AAAA C
ATOM	3229	CD1	ILE	340	28.897	49.634	31.915	1.00 92.53	AAAA C
ATOM	3230	C	ILE	340	28.783	50.357	35.706	1.00 95.32	AAAA C
ATOM	3231	O	ILE	340	29.472	51.099	34.997	1.00 97.86	AAAA O
ATOM	3232	N	ALA	341	28.409	50.739	36.915	1.00 89.89	AAAA N
ATOM	3234	CA	ALA	341	28.892	52.008	37.450	1.00 88.45	AAAA C
ATOM	3235	CB	ALA	341	28.068	53.201	37.006	1.00 84.56	AAAA C
ATOM	3236	C	ALA	341	28.786	51.968	38.970	1.00 85.37	AAAA C
ATOM	3237	O	ALA	341	28.910	52.935	39.690	1.00 86.09	AAAA O
ATOM	3238	N	SER	342	28.204	50.877	39.386	1.00 84.24	AAAA N
ATOM	3240	CA	SER	342	27.910	50.601	40.780	1.00 82.05	AAAA C
ATOM	3241	CB	SER	342	26.426	50.667	41.112	1.00 85.51	AAAA C
ATOM	3242	OG	SER	342	26.145	51.271	42.361	1.00 86.02	AAAA O
ATOM	3244	C	SER	342	28.487	49.196	40.965	1.00 76.62	AAAA C
ATOM	3245	O	SER	342	29.119	48.966	41.964	1.00 71.76	AAAA O
ATOM	3246	N	GLU	343	28.373	48.409	39.905	1.00 76.23	AAAA N
ATOM	3248	CA	GLU	343	29.001	47.109	39.820	1.00 74.59	AAAA C
ATOM	3249	CB	GLU	343	28.595	46.300	38.616	1.00 78.62	AAAA C
ATOM	3250	CG	GLU	343	27.118	46.105	38.316	1.00 85.33	AAAA C
ATOM	3251	CD	GLU	343	26.898	45.121	37.169	1.00 92.76	AAAA C
ATOM	3252	OE1	GLU	343	27.209	43.911	37.310	1.00 96.41	AAAA O
ATOM	3253	OE2	GLU	343	26.423	45.517	36.082	1.00 98.55	AAAA O
ATOM	3254	C	GLU	343	30.525	47.319	39.804	1.00 77.75	AAAA C
ATOM	3255	O	GLU	343	31.273	46.787	40.637	1.00 75.73	AAAA O
ATOM	3256	N	LEU	344	31.022	48.237	38.966	1.00 75.65	AAAA N
ATOM	3258	CA	LEU	344	32.415	48.596	38.839	1.00 72.36	AAAA C
ATOM	3259	CB	LEU	344	32.760	49.697	37.808	1.00 64.33	AAAA C
ATOM	3260	CG	LEU	344	32.687	49.397	36.311	1.00 50.12	AAAA C
ATOM	3261	CD1	LEU	344	33.224	50.577	35.519	1.00 57.00	AAAA C
ATOM	3262	CD2	LEU	344	33.401	48.127	35.905	1.00 51.62	AAAA C
ATOM	3263	C	LEU	344	32.963	49.130	40.174	1.00 69.74	AAAA C
ATOM	3264	O	LEU	344	34.079	48.739	40.551	1.00 69.12	AAAA O
ATOM	3265	N	GLU	345	32.166	49.959	40.822	1.00 63.10	AAAA N
ATOM	3267	CA	GLU	345	32.555	50.591	42.061	1.00 65.42	AAAA C
ATOM	3268	CB	GLU	345	31.592	51.714	42.478	1.00 55.59	AAAA C
ATOM	3269	CG	GLU	345	32.267	52.607	43.486	1.00 68.78	AAAA C
ATOM	3270	CD	GLU	345	31.324	53.374	44.376	1.00 81.31	AAAA C
ATOM	3271	OE1	GLU	345	30.614	54.320	43.976	1.00 85.60	AAAA O
ATOM	3272	OE2	GLU	345	31.237	53.078	45.595	1.00 88.79	AAAA O
ATOM	3273	C	GLU	345	32.706	49.652	43.255	1.00 63.31	AAAA C
ATOM	3274	O	GLU	345	33.501	49.913	44.134	1.00 60.06	AAAA O
ATOM	3275	N	ASN	346	32.151	48.462	43.202	1.00 62.25	AAAA N
ATOM	3277	CA	ASN	346	32.285	47.403	44.173	1.00 63.82	AAAA C
ATOM	3278	CB	ASN	346	31.024	46.498	44.095	1.00 61.66	AAAA C
ATOM	3279	CG	ASN	346	31.110	45.292	45.006	1.00 58.73	AAAA C
ATOM	3280	OD1	ASN	346	31.188	45.352	46.224	1.00 69.11	AAAA O
ATOM	3281	ND2	ASN	346	31.155	44.092	44.444	1.00 51.10	AAAA N
ATOM	3284	C	ASN	346	33.532	46.580	43.870	1.00 63.71	AAAA C
ATOM	3285	O	ASN	346	33.636	45.336	43.905	1.00 65.65	AAAA O
ATOM	3286	N	PHE	347	34.419	47.173	43.066	1.00 63.23	AAAA N
ATOM	3288	CA	PHE	347	35.540	46.411	42.506	1.00 61.39	AAAA C
ATOM	3289	CB	PHE	347	35.123	45.854	41.170	1.00 61.38	AAAA C
ATOM	3290	CG	PHE	347	34.457	44.534	41.142	1.00 65.57	AAAA C
ATOM	3291	CD1	PHE	347	33.090	44.438	40.982	1.00 75.25	AAAA C
ATOM	3292	CD2	PHE	347	35.148	43.351	41.267	1.00 77.15	AAAA C
ATOM	3293	CE1	PHE	347	32.425	43.224	40.951	1.00 75.55	AAAA C
ATOM	3294	CE2	PHE	347	34.512	42.130	41.249	1.00 72.86	AAAA C
ATOM	3295	CZ	PHE	347	33.152	42.051	41.095	1.00 72.74	AAAA C
ATOM	3296	C	PHE	347	36.712	47.375	42.440	1.00 57.70	AAAA C
ATOM	3297	O	PHE	347	37.770	46.820	42.354	1.00 59.92	AAAA O
ATOM	3298	N	MET	348	36.482	48.676	42.319	1.00 50.56	AAAA N
ATOM	3300	CA	MET	348	37.500	49.630	41.964	1.00 42.86	AAAA C
ATOM	3301	CB	MET	348	37.402	50.096	40.493	1.00 31.72	AAAA C
ATOM	3302	CG	MET	348	37.426	48.933	39.471	1.00 33.42	AAAA C
ATOM	3303	SD	MET	348	37.566	49.448	37.732	1.00 44.79	AAAA S
ATOM	3304	CE	MET	348	38.408	50.999	37.791	1.00 59.57	AAAA C
ATOM	3305	C	MET	348	37.368	50.831	42.867	1.00 45.88	AAAA C
ATOM	3306	O	MET	348	38.210	51.772	42.901	1.00 43.33	AAAA O
ATOM	3307	N	GLY	349	36.296	50.783	43.683	1.00 45.30	AAAA N
ATOM	3309	CA	GLY	349	35.998	51.965	44.504	1.00 49.19	AAAA C
ATOM	3310	C	GLY	349	36.980	52.189	45.620	1.00 52.77	AAAA C
ATOM	3311	O	GLY	349	37.033	53.299	46.156	1.00 53.43	AAAA O

ATOM	3312	N	LEU	350	37.791	51.159	45.925	1.00	56.17	AAAA N
ATOM	3314	CA	LEU	350	38.735	51.256	47.021	1.00	58.04	AAAA C
ATOM	3315	CB	LEU	350	38.873	49.949	47.834	1.00	49.00	AAAA C
ATOM	3316	CG	LEU	350	37.871	50.020	49.031	1.00	50.79	AAAA C
ATOM	3317	CD1	LEU	350	37.705	48.680	49.700	1.00	52.92	AAAA C
ATOM	3318	CD2	LEU	350	38.247	51.106	50.038	1.00	56.11	AAAA C
ATOM	3319	C	LEU	350	40.144	51.727	46.685	1.00	61.34	AAAA C
ATOM	3320	O	LEU	350	40.931	51.962	47.618	1.00	63.52	AAAA O
ATOM	3321	N	ILE	351	40.446	51.677	45.372	1.00	57.89	AAAA N
ATOM	3323	CA	ILE	351	41.729	52.088	44.873	1.00	48.69	AAAA C
ATOM	3324	CB	ILE	351	41.814	51.912	43.352	1.00	48.19	AAAA C
ATOM	3325	CG2	ILE	351	43.121	52.416	42.757	1.00	40.01	AAAA C
ATOM	3326	CG1	ILE	351	41.535	50.418	43.058	1.00	36.87	AAAA C
ATOM	3327	CD1	ILE	351	41.172	50.351	41.581	1.00	36.46	AAAA C
ATOM	3328	C	ILE	351	42.031	53.533	45.178	1.00	46.80	AAAA C
ATOM	3329	O	ILE	351	41.367	54.358	44.626	1.00	42.87	AAAA O
ATOM	3330	N	GLU	352	43.002	53.866	46.015	1.00	50.61	AAAA N
ATOM	3332	CA	GLU	352	43.381	55.241	46.248	1.00	51.20	AAAA C
ATOM	3333	CB	GLU	352	43.907	55.353	47.678	1.00	52.12	AAAA C
ATOM	3334	CG	GLU	352	42.912	55.769	48.735	1.00	65.55	AAAA C
ATOM	3335	CD	GLU	352	43.034	54.834	49.947	1.00	71.49	AAAA C
ATOM	3336	OE1	GLU	352	43.881	55.244	50.765	1.00	66.09	AAAA O
ATOM	3337	OE2	GLU	352	42.330	53.799	50.009	1.00	76.07	AAAA O
ATOM	3338	C	GLU	352	44.502	55.751	45.314	1.00	47.43	AAAA C
ATOM	3339	O	GLU	352	44.798	56.951	45.182	1.00	40.38	AAAA O
ATOM	3340	N	VAL	353	45.342	54.838	44.852	1.00	43.54	AAAA N
ATOM	3342	CA	VAL	353	46.512	55.236	44.078	1.00	43.71	AAAA C
ATOM	3343	CB	VAL	353	47.759	55.540	44.911	1.00	45.01	AAAA C
ATOM	3344	CG1	VAL	353	47.766	55.261	46.387	1.00	30.84	AAAA C
ATOM	3345	CG2	VAL	353	48.988	54.844	44.319	1.00	42.55	AAAA C
ATOM	3346	C	VAL	353	46.828	54.233	42.957	1.00	41.41	AAAA C
ATOM	3347	O	VAL	353	46.843	53.003	43.172	1.00	39.19	AAAA O
ATOM	3348	N	VAL	354	47.074	54.855	41.816	1.00	36.31	AAAA N
ATOM	3350	CA	VAL	354	47.586	54.092	40.651	1.00	43.97	AAAA C
ATOM	3351	CB	VAL	354	46.725	54.390	39.407	1.00	40.86	AAAA C
ATOM	3352	CG1	VAL	354	47.347	53.896	38.123	1.00	36.72	AAAA C
ATOM	3353	CG2	VAL	354	45.293	53.849	39.678	1.00	35.35	AAAA C
ATOM	3354	C	VAL	354	49.043	54.510	40.388	1.00	44.56	AAAA C
ATOM	3355	O	VAL	354	49.366	55.718	40.288	1.00	43.32	AAAA O
ATOM	3356	N	THR	355	49.972	53.561	40.431	1.00	43.83	AAAA N
ATOM	3358	CA	THR	355	51.392	53.914	40.284	1.00	44.85	AAAA C
ATOM	3359	CB	THR	355	52.374	52.799	40.653	1.00	42.40	AAAA C
ATOM	3360	OG1	THR	355	52.273	51.744	39.695	1.00	45.30	AAAA O
ATOM	3362	CG2	THR	355	52.210	52.194	42.039	1.00	38.13	AAAA C
ATOM	3363	C	THR	355	51.746	54.339	38.851	1.00	43.84	AAAA C
ATOM	3364	O	THR	355	52.463	55.334	38.697	1.00	44.26	AAAA O
ATOM	3365	N	GLY	356	51.127	53.704	37.870	1.00	41.16	AAAA N
ATOM	3367	CA	GLY	356	51.358	54.073	36.479	1.00	37.91	AAAA C
ATOM	3368	C	GLY	356	50.505	55.204	35.955	1.00	38.07	AAAA C
ATOM	3369	O	GLY	356	50.364	56.261	36.615	1.00	34.65	AAAA O
ATOM	3370	N	TYR	357	49.910	55.004	34.800	1.00	38.47	AAAA N
ATOM	3372	CA	TYR	357	48.982	55.973	34.205	1.00	38.03	AAAA C
ATOM	3373	CB	TYR	357	49.557	56.343	32.805	1.00	31.44	AAAA C
ATOM	3374	CG	TYR	357	49.473	55.219	31.812	1.00	33.04	AAAA C
ATOM	3375	CD1	TYR	357	48.333	54.842	31.077	1.00	32.86	AAAA C
ATOM	3376	CE1	TYR	357	48.352	53.779	30.175	1.00	32.83	AAAA C
ATOM	3377	CD2	TYR	357	50.639	54.465	31.606	1.00	34.28	AAAA C
ATOM	3378	CE2	TYR	357	50.706	53.402	30.720	1.00	32.51	AAAA C
ATOM	3379	CZ	TYR	357	49.552	53.068	30.007	1.00	37.26	AAAA C
ATOM	3380	OH	TYR	357	49.726	51.997	29.166	1.00	35.85	AAAA O
ATOM	3382	C	TYR	357	47.582	55.368	34.150	1.00	38.55	AAAA C
ATOM	3383	O	TYR	357	47.458	54.127	34.088	1.00	36.11	AAAA O
ATOM	3384	N	VAL	358	46.593	56.216	33.814	1.00	40.98	AAAA N
ATOM	3386	CA	VAL	358	45.197	55.798	33.639	1.00	38.90	AAAA C
ATOM	3387	CB	VAL	358	44.211	56.502	34.610	1.00	49.15	AAAA C
ATOM	3388	CG1	VAL	358	42.815	55.883	34.484	1.00	33.12	AAAA C
ATOM	3389	CG2	VAL	358	44.748	56.437	36.043	1.00	29.20	AAAA C
ATOM	3390	C	VAL	358	44.760	56.194	32.234	1.00	35.64	AAAA C
ATOM	3391	O	VAL	358	44.792	57.358	31.885	1.00	34.58	AAAA O
ATOM	3392	N	LYS	359	44.387	55.188	31.461	1.00	36.00	AAAA N
ATOM	3394	CA	LYS	359	43.898	55.419	30.117	1.00	41.27	AAAA C
ATOM	3395	CB	LYS	359	44.845	54.707	29.174	1.00	37.40	AAAA C
ATOM	3396	CG	LYS	359	44.340	54.473	27.770	1.00	45.19	AAAA C
ATOM	3397	CD	LYS	359	45.040	55.317	26.750	1.00	43.40	AAAA C
ATOM	3398	CE	LYS	359	45.958	54.402	25.986	1.00	43.56	AAAA C
ATOM	3399	NZ	LYS	359	45.416	53.937	24.680	1.00	47.98	AAAA N
ATOM	3403	C	LYS	359	42.423	54.979	29.939	1.00	42.14	AAAA C
ATOM	3404	O	LYS	359	42.056	53.791	30.006	1.00	40.40	AAAA O
ATOM	3405	N	ILE	360	41.602	55.974	29.572	1.00	37.16	AAAA N
ATOM	3407	CA	ILE	360	40.164	55.742	29.334	1.00	40.02	AAAA C
ATOM	3408	CB	ILE	360	39.297	56.804	30.048	1.00	38.10	AAAA C
ATOM	3409	CG2	ILE	360	37.887	56.277	29.932	1.00	39.42	AAAA C
ATOM	3410	CG1	ILE	360	39.769	57.111	31.481	1.00	28.54	AAAA C
ATOM	3411	CD1	ILE	360	39.423	56.037	32.491	1.00	33.16	AAAA C
ATOM	3412	C	ILE	360	39.888	55.837	27.834	1.00	39.49	AAAA C

ATOM	3413	O	ILE	360	40.014	56.942	27.235	1.00	37.32	AAAA O
ATOM	3414	N	ARG	361	39.567	54.721	27.221	1.00	34.34	AAAA N
ATOM	3416	CA	ARG	361	39.472	54.782	25.744	1.00	41.24	AAAA C
ATOM	3417	CB	ARG	361	40.783	54.213	25.148	1.00	47.92	AAAA C
ATOM	3418	CG	ARG	361	40.805	54.203	23.646	1.00	50.39	AAAA C
ATOM	3419	CD	ARG	361	41.943	53.357	23.116	1.00	51.36	AAAA C
ATOM	3420	NE	ARG	361	41.473	51.974	23.263	1.00	50.97	AAAA N
ATOM	3422	CZ	ARG	361	42.297	50.962	23.490	1.00	55.78	AAAA C
ATOM	3423	NH1	ARG	361	43.612	51.074	23.616	1.00	51.62	AAAA N
ATOM	3426	NH2	ARG	361	41.834	49.719	23.631	1.00	54.52	AAAA N
ATOM	3429	C	ARG	361	38.382	53.866	25.246	1.00	42.06	AAAA C
ATOM	3430	O	ARG	361	38.336	52.661	25.499	1.00	38.93	AAAA O
ATOM	3431	N	HIS	362	37.514	54.342	24.373	1.00	46.19	AAAA N
ATOM	3433	CA	HIS	362	36.372	53.555	23.885	1.00	49.34	AAAA C
ATOM	3434	CB	HIS	362	37.000	52.300	23.266	1.00	40.94	AAAA C
ATOM	3435	CG	HIS	362	37.849	52.610	22.084	1.00	42.78	AAAA C
ATOM	3436	CD2	HIS	362	38.049	53.765	21.411	1.00	48.32	AAAA C
ATOM	3437	ND1	HIS	362	38.628	51.676	21.469	1.00	43.59	AAAA N
ATOM	3439	CE1	HIS	362	39.256	52.247	20.465	1.00	46.01	AAAA C
ATOM	3440	NE2	HIS	362	38.923	53.515	20.408	1.00	49.22	AAAA N
ATOM	3442	C	HIS	362	35.295	53.113	24.913	1.00	50.32	AAAA C
ATOM	3443	O	HIS	362	34.686	52.030	24.795	1.00	41.31	AAAA O
ATOM	3444	N	SER	363	35.222	53.875	26.013	1.00	46.96	AAAA N
ATOM	3446	CA	SER	363	34.402	53.456	27.139	1.00	52.19	AAAA C
ATOM	3447	CB	SER	363	35.231	53.837	28.400	1.00	53.73	AAAA C
ATOM	3448	OG	SER	363	35.713	52.558	28.816	1.00	41.72	AAAA O
ATOM	3450	C	SER	363	33.005	54.072	27.046	1.00	49.08	AAAA C
ATOM	3451	O	SER	363	32.653	55.040	27.694	1.00	37.49	AAAA O
ATOM	3452	N	HIS	364	32.243	53.577	26.058	1.00	52.25	AAAA N
ATOM	3454	CA	HIS	364	30.954	54.173	25.717	1.00	53.66	AAAA C
ATOM	3455	C	HIS	364	29.879	53.937	26.760	1.00	48.77	AAAA C
ATOM	3456	O	HIS	364	29.297	54.899	27.280	1.00	51.44	AAAA O
ATOM	3457	CB	HIS	364	30.485	53.699	24.348	1.00	49.83	AAAA C
ATOM	3458	CG	HIS	364	31.493	54.182	23.338	1.00	51.51	AAAA C
ATOM	3459	ND1	HIS	364	31.870	55.502	23.156	1.00	44.83	AAAA N
ATOM	3460	CE1	HIS	364	32.798	55.533	22.214	1.00	28.57	AAAA C
ATOM	3461	CD2	HIS	364	32.194	53.393	22.472	1.00	38.62	AAAA C
ATOM	3462	NE2	HIS	364	32.992	54.274	21.810	1.00	41.44	AAAA N
ATOM	3464	N	ALA	365	29.949	52.819	27.427	1.00	47.53	AAAA N
ATOM	3466	CA	ALA	365	29.211	52.488	28.621	1.00	44.41	AAAA C
ATOM	3467	CB	ALA	365	29.678	51.133	29.150	1.00	40.28	AAAA C
ATOM	3468	C	ALA	365	29.318	53.473	29.768	1.00	44.70	AAAA C
ATOM	3469	O	ALA	365	28.576	53.206	30.726	1.00	45.28	AAAA O
ATOM	3470	N	LEU	366	30.158	54.517	29.762	1.00	40.80	AAAA N
ATOM	3472	CA	LEU	366	30.415	55.243	30.968	1.00	42.21	AAAA C
ATOM	3473	CB	LEU	366	31.885	55.241	31.350	1.00	43.78	AAAA C
ATOM	3474	CG	LEU	366	32.740	54.037	31.667	1.00	51.52	AAAA C
ATOM	3475	CD1	LEU	366	34.192	54.373	32.043	1.00	51.77	AAAA C
ATOM	3476	CD2	LEU	366	32.118	53.305	32.834	1.00	51.17	AAAA C
ATOM	3477	C	LEU	366	29.974	56.687	30.896	1.00	46.36	AAAA C
ATOM	3478	O	LEU	366	30.305	57.248	29.849	1.00	48.40	AAAA O
ATOM	3479	N	VAL	367	29.521	57.275	32.015	1.00	43.68	AAAA N
ATOM	3481	CA	VAL	367	29.072	58.675	31.940	1.00	44.18	AAAA C
ATOM	3482	CB	VAL	367	27.557	58.727	32.376	1.00	48.80	AAAA C
ATOM	3483	CG1	VAL	367	26.923	60.073	32.571	1.00	41.69	AAAA C
ATOM	3484	CG2	VAL	367	26.697	57.949	31.365	1.00	34.00	AAAA C
ATOM	3485	C	VAL	367	29.923	59.518	32.845	1.00	44.90	AAAA C
ATOM	3486	O	VAL	367	29.965	60.751	32.720	1.00	44.75	AAAA O
ATOM	3487	N	SER	368	30.591	58.818	33.757	1.00	48.72	AAAA N
ATOM	3489	CA	SER	368	31.487	59.465	34.742	1.00	52.70	AAAA C
ATOM	3490	CB	SER	368	30.658	59.706	36.000	1.00	55.32	AAAA C
ATOM	3491	OG	SER	368	31.300	60.298	37.091	1.00	64.86	AAAA O
ATOM	3493	C	SER	368	32.590	58.497	35.179	1.00	52.76	AAAA C
ATOM	3494	O	SER	368	32.352	57.299	34.976	1.00	48.99	AAAA O
ATOM	3495	N	LEU	369	33.631	59.012	35.831	1.00	53.86	AAAA N
ATOM	3497	CA	LEU	369	34.716	58.129	36.274	1.00	60.15	AAAA C
ATOM	3498	CB	LEU	369	36.073	58.630	35.784	1.00	55.91	AAAA C
ATOM	3499	CG	LEU	369	36.325	58.736	34.271	1.00	45.96	AAAA C
ATOM	3500	CD1	LEU	369	37.669	59.428	34.154	1.00	53.97	AAAA C
ATOM	3501	CD2	LEU	369	36.207	57.384	33.619	1.00	38.77	AAAA C
ATOM	3502	C	LEU	369	34.645	58.036	37.811	1.00	62.52	AAAA C
ATOM	3503	O	LEU	369	35.569	57.700	38.595	1.00	59.33	AAAA O
ATOM	3504	N	SER	370	33.437	58.401	38.285	1.00	56.26	AAAA N
ATOM	3506	CA	SER	370	33.089	58.431	39.690	1.00	53.88	AAAA C
ATOM	3507	CB	SER	370	31.673	59.052	39.816	1.00	57.50	AAAA C
ATOM	3508	OG	SER	370	30.771	58.061	39.261	1.00	69.12	AAAA O
ATOM	3510	C	SER	370	33.060	57.085	40.412	1.00	47.97	AAAA C
ATOM	3511	O	SER	370	33.228	56.943	41.596	1.00	41.93	AAAA O
ATOM	3512	N	PHE	371	32.967	55.936	39.792	1.00	45.48	AAAA N
ATOM	3514	CA	PHE	371	33.223	54.643	40.356	1.00	46.29	AAAA C
ATOM	3515	CB	PHE	371	32.952	53.596	39.287	1.00	43.53	AAAA C
ATOM	3516	CG	PHE	371	33.724	53.629	38.012	1.00	56.45	AAAA C
ATOM	3517	CD1	PHE	371	34.805	52.807	37.764	1.00	58.95	AAAA C
ATOM	3518	CD2	PHE	371	33.371	54.515	37.004	1.00	53.92	AAAA C
ATOM	3519	CE1	PHE	371	35.498	52.842	36.570	1.00	59.50	AAAA C

ATOM	3520	CE2	PHE	371	34.948	54.546	35.817	1.00	56.49	AAAA C
ATOM	3521	CZ	PHE	371	35.119	53.716	35.579	1.00	56.39	AAAA C
ATOM	3522	C	PHE	371	34.654	54.467	40.895	1.00	54.84	AAAA C
ATOM	3523	O	PHE	371	35.005	53.592	41.728	1.00	52.23	AAAA O
ATOM	3524	N	LEU	372	35.633	55.305	40.510	1.00	50.17	AAAA N
ATOM	3526	CA	LEU	372	36.928	55.395	41.109	1.00	46.25	AAAA C
ATOM	3527	CB	LEU	372	38.171	55.812	40.276	1.00	44.82	AAAA C
ATOM	3528	CG	LEU	372	38.411	54.800	39.114	1.00	36.78	AAAA C
ATOM	3529	CD1	LEU	372	38.853	55.643	37.934	1.00	45.04	AAAA C
ATOM	3530	CD2	LEU	372	39.260	53.657	39.565	1.00	35.55	AAAA C
ATOM	3531	C	LEU	372	36.715	56.392	42.243	1.00	42.26	AAAA C
ATOM	3532	O	LEU	372	37.224	57.507	42.364	1.00	38.37	AAAA O
ATOM	3533	N	LYS	373	35.970	55.862	43.192	1.00	47.06	AAAA N
ATOM	3535	CA	LYS	373	35.527	56.509	44.415	1.00	50.19	AAAA C
ATOM	3536	CB	LYS	373	34.546	55.521	45.077	1.00	56.74	AAAA C
ATOM	3537	CG	LYS	373	33.645	56.162	46.119	1.00	59.64	AAAA C
ATOM	3538	CD	LYS	373	32.529	56.955	45.441	0.01	60.17	AAAA C
ATOM	3539	CE	LYS	373	31.674	57.687	46.460	0.01	60.45	AAAA C
ATOM	3540	NZ	LYS	373	31.083	58.933	45.899	0.01	60.38	AAAA N
ATOM	3544	C	LYS	373	36.646	56.863	45.366	1.00	49.72	AAAA C
ATOM	3545	O	LYS	373	36.636	57.960	45.907	1.00	42.42	AAAA O
ATOM	3546	N	ASN	374	37.657	55.986	45.513	1.00	54.43	AAAA N
ATOM	3548	CA	ASN	374	38.765	56.352	46.410	1.00	59.92	AAAA C
ATOM	3549	CB	ASN	374	39.080	55.154	47.314	1.00	63.16	AAAA C
ATOM	3550	CG	ASN	374	38.009	54.978	48.396	1.00	64.53	AAAA C
ATOM	3551	OD1	ASN	374	37.892	53.972	49.096	1.00	66.40	AAAA O
ATOM	3552	ND2	ASN	374	37.160	55.965	48.578	1.00	52.88	AAAA N
ATOM	3555	C	ASN	374	40.043	56.892	45.786	1.00	62.35	AAAA C
ATOM	3556	O	ASN	374	41.031	57.223	46.479	1.00	63.08	AAAA O
ATOM	3557	N	LEU	375	40.091	56.893	44.438	1.00	58.34	AAAA N
ATOM	3559	CA	LEU	375	41.305	57.374	43.795	1.00	54.73	AAAA C
ATOM	3560	CB	LEU	375	41.099	57.359	42.288	1.00	56.41	AAAA C
ATOM	3561	CG	LEU	375	42.396	57.422	41.459	1.00	54.12	AAAA C
ATOM	3562	CD1	LEU	375	43.135	56.112	41.689	1.00	37.88	AAAA C
ATOM	3563	CD2	LEU	375	42.030	57.796	40.041	1.00	40.97	AAAA C
ATOM	3564	C	LEU	375	41.712	58.754	44.245	1.00	52.37	AAAA C
ATOM	3565	O	LEU	375	41.151	59.777	43.877	1.00	52.11	AAAA O
ATOM	3566	N	ARG	376	42.801	58.874	44.982	1.00	55.16	AAAA N
ATOM	3568	CA	ARG	376	43.320	60.155	45.434	1.00	55.45	AAAA C
ATOM	3569	CB	ARG	376	43.706	60.222	46.928	1.00	58.68	AAAA C
ATOM	3570	CG	ARG	376	44.288	58.907	47.415	1.00	69.10	AAAA C
ATOM	3571	CD	ARG	376	44.286	58.817	48.944	1.00	81.17	AAAA C
ATOM	3572	NE	ARG	376	45.377	57.926	49.410	1.00	84.46	AAAA N
ATOM	3574	CZ	ARG	376	46.618	58.380	49.598	1.00	85.64	AAAA C
ATOM	3575	NH1	ARG	376	46.966	59.645	49.383	1.00	81.84	AAAA N
ATOM	3578	NH2	ARG	376	47.571	57.548	50.012	1.00	94.15	AAAA N
ATOM	3581	C	ARG	376	44.556	60.544	44.633	1.00	50.16	AAAA C
ATOM	3582	O	ARG	376	44.746	61.728	44.465	1.00	44.25	AAAA O
ATOM	3583	N	LEU	377	45.375	59.578	44.219	1.00	50.99	AAAA N
ATOM	3585	CA	LEU	377	46.526	59.942	43.379	1.00	49.40	AAAA C
ATOM	3586	CB	LEU	377	47.596	60.411	44.329	1.00	64.72	AAAA C
ATOM	3587	CG	LEU	377	48.806	59.577	44.667	1.00	70.76	AAAA C
ATOM	3588	CD1	LEU	377	50.031	60.157	43.954	1.00	63.32	AAAA C
ATOM	3589	CD2	LEU	377	49.010	59.696	46.179	1.00	68.60	AAAA C
ATOM	3590	C	LEU	377	47.043	59.022	42.311	1.00	46.33	AAAA C
ATOM	3591	O	LEU	377	46.868	57.788	42.286	1.00	45.17	AAAA O
ATOM	3592	N	ILE	378	47.448	59.675	41.199	1.00	45.12	AAAA N
ATOM	3594	CA	ILE	378	48.042	58.976	40.042	1.00	49.10	AAAA C
ATOM	3595	CB	ILE	378	47.342	59.303	38.724	1.00	46.36	AAAA C
ATOM	3596	CG2	ILE	378	48.115	58.696	37.574	1.00	34.36	AAAA C
ATOM	3597	CG1	ILE	378	45.871	58.862	38.829	1.00	38.59	AAAA C
ATOM	3598	CD1	ILE	378	44.999	59.515	37.765	1.00	37.18	AAAA C
ATOM	3599	C	ILE	378	49.524	59.381	40.003	1.00	49.87	AAAA C
ATOM	3600	O	ILE	378	49.801	60.595	40.040	1.00	44.72	AAAA O
ATOM	3601	N	LEU	379	50.454	58.423	40.067	1.00	49.97	AAAA N
ATOM	3603	CA	LEU	379	51.866	58.712	40.344	1.00	48.48	AAAA C
ATOM	3604	CB	LEU	379	52.575	57.531	41.054	1.00	48.44	AAAA C
ATOM	3605	CG	LEU	379	52.234	57.363	42.554	1.00	50.28	AAAA C
ATOM	3606	CD1	LEU	379	52.926	56.187	43.217	1.00	39.89	AAAA C
ATOM	3607	CD2	LEU	379	52.616	58.625	43.300	1.00	42.89	AAAA C
ATOM	3608	C	LEU	379	52.609	59.019	39.080	1.00	50.94	AAAA C
ATOM	3609	O	LEU	379	53.576	59.788	39.139	1.00	54.23	AAAA O
ATOM	3610	N	GLY	380	52.175	58.423	37.972	1.00	48.67	AAAA N
ATOM	3612	CA	GLY	380	52.931	58.715	36.702	1.00	49.94	AAAA C
ATOM	3613	C	GLY	380	54.249	58.155	36.624	1.00	52.70	AAAA C
ATOM	3614	O	GLY	380	55.026	58.657	35.803	1.00	49.94	AAAA O
ATOM	3615	N	GLU	381	54.549	57.033	37.272	1.00	52.51	AAAA N
ATOM	3617	CA	GLU	381	55.849	56.386	37.243	1.00	52.33	AAAA C
ATOM	3618	CB	GLU	381	56.055	55.310	38.323	1.00	45.22	AAAA C
ATOM	3619	CG	GLU	381	55.402	55.779	39.636	1.00	52.91	AAAA C
ATOM	3620	CD	GLU	381	56.050	55.192	40.873	1.00	42.11	AAAA C
ATOM	3621	OE1	GLU	381	56.160	53.966	40.890	1.00	40.26	AAAA O
ATOM	3622	OE2	GLU	381	56.379	56.014	41.754	1.00	51.32	AAAA O
ATOM	3623	C	GLU	381	56.078	55.784	35.859	1.00	55.86	AAAA C
ATOM	3624	O	GLU	381	57.216	55.652	35.345	1.00	54.61	AAAA O

ATOM	3625	N	GLU	382	54.980	55.449	35.157	1.00	53.56	AAAA N
ATOM	3627	CA	GLU	382	55.091	55.018	33.766	1.00	48.15	AAAA C
ATOM	3628	CB	GLU	382	55.051	53.550	33.532	1.00	35.27	AAAA C
ATOM	3629	CG	GLU	382	54.739	53.225	32.051	1.00	49.69	AAAA C
ATOM	3630	CD	GLU	382	54.676	51.719	31.807	1.00	56.45	AAAA C
ATOM	3631	OE1	GLU	382	55.062	50.924	32.705	1.00	61.66	AAAA O
ATOM	3632	OE2	GLU	382	54.264	51.201	30.745	1.00	57.69	AAAA O
ATOM	3633	C	GLU	382	54.006	55.732	32.973	1.00	50.84	AAAA C
ATOM	3634	O	GLU	382	53.097	56.282	33.598	1.00	49.44	AAAA O
ATOM	3635	N	GLN	383	54.347	56.256	31.780	1.00	52.25	AAAA N
ATOM	3637	CA	GLN	383	53.498	57.153	31.016	1.00	40.15	AAAA C
ATOM	3638	CB	GLN	383	53.914	58.609	31.155	1.00	28.50	AAAA C
ATOM	3639	CG	GLN	383	54.489	58.909	32.542	1.00	31.10	AAAA C
ATOM	3640	CD	GLN	383	54.950	60.301	32.752	1.00	33.19	AAAA C
ATOM	3641	OE1	GLN	383	55.186	60.840	31.683	1.00	40.34	AAAA O
ATOM	3642	NE2	GLN	383	55.043	60.943	33.934	1.00	36.30	AAAA N
ATOM	3645	C	GLN	383	53.426	56.744	29.563	1.00	40.45	AAAA C
ATOM	3646	O	GLN	383	54.131	55.858	29.139	1.00	43.45	AAAA O
ATOM	3647	N	LEU	384	52.375	57.195	28.860	1.00	42.54	AAAA N
ATOM	3649	CA	LEU	384	52.257	56.889	27.443	1.00	43.24	AAAA C
ATOM	3650	CB	LEU	384	50.814	57.011	26.949	1.00	43.79	AAAA C
ATOM	3651	CG	LEU	384	49.818	56.235	27.861	1.00	41.21	AAAA C
ATOM	3652	CD1	LEU	384	48.611	57.095	28.221	1.00	33.99	AAAA C
ATOM	3653	CD2	LEU	384	49.405	54.968	27.149	1.00	33.20	AAAA C
ATOM	3654	C	LEU	384	53.204	57.809	26.672	1.00	40.51	AAAA C
ATOM	3655	O	LEU	384	53.582	58.872	27.177	1.00	29.66	AAAA O
ATOM	3656	N	GLU	385	53.659	57.319	25.531	1.00	45.22	AAAA N
ATOM	3658	CA	GLU	385	54.410	58.116	24.570	1.00	49.98	AAAA C
ATOM	3659	CB	GLU	385	54.424	57.475	23.174	1.00	60.50	AAAA C
ATOM	3660	CG	GLU	385	55.045	56.095	23.106	1.00	68.76	AAAA C
ATOM	3661	CD	GLU	385	54.195	54.951	23.592	1.00	72.07	AAAA C
ATOM	3662	OE1	GLU	385	53.150	55.213	24.244	1.00	81.88	AAAA O
ATOM	3663	OE2	GLU	385	54.565	53.786	23.301	1.00	73.13	AAAA O
ATOM	3664	C	GLU	385	53.828	59.515	24.450	1.00	47.41	AAAA C
ATOM	3665	O	GLU	385	52.635	59.706	24.184	1.00	54.43	AAAA O
ATOM	3666	N	GLY	386	54.614	60.470	24.902	1.00	43.69	AAAA N
ATOM	3668	CA	GLY	386	54.181	61.870	24.897	1.00	40.34	AAAA C
ATOM	3669	C	GLY	386	54.286	62.449	26.308	1.00	40.65	AAAA C
ATOM	3670	O	GLY	386	53.930	63.615	26.491	1.00	39.75	AAAA O
ATOM	3671	N	ASN	387	54.441	61.537	27.272	1.00	40.75	AAAA N
ATOM	3673	CA	ASN	387	54.479	61.912	28.675	1.00	49.18	AAAA C
ATOM	3674	CB	ASN	387	55.500	63.084	28.874	1.00	44.41	AAAA C
ATOM	3675	CG	ASN	387	56.925	62.541	28.722	1.00	61.51	AAAA C
ATOM	3676	OD1	ASN	387	57.199	61.313	28.677	1.00	57.85	AAAA O
ATOM	3677	ND2	ASN	387	58.063	63.251	28.592	1.00	61.96	AAAA N
ATOM	3680	C	ASN	387	53.095	62.100	29.299	1.00	48.46	AAAA C
ATOM	3681	O	ASN	387	52.836	62.891	30.218	1.00	48.99	AAAA O
ATOM	3682	N	TYR	388	52.214	61.116	29.058	1.00	46.29	AAAA N
ATOM	3684	CA	TYR	388	50.846	61.199	29.540	1.00	45.09	AAAA C
ATOM	3685	CB	TYR	388	49.823	60.957	28.399	1.00	40.70	AAAA C
ATOM	3686	CG	TYR	388	49.925	62.056	27.373	1.00	42.24	AAAA C
ATOM	3687	CD1	TYR	388	50.343	61.854	26.064	1.00	44.39	AAAA C
ATOM	3688	CE1	TYR	388	50.401	62.885	25.157	1.00	35.51	AAAA C
ATOM	3689	CD2	TYR	388	49.625	63.356	27.709	1.00	44.67	AAAA C
ATOM	3690	CE2	TYR	388	49.699	64.428	26.830	1.00	38.14	AAAA C
ATOM	3691	CZ	TYR	388	50.087	64.148	25.555	1.00	41.27	AAAA C
ATOM	3692	OH	TYR	388	50.151	65.181	24.604	1.00	50.18	AAAA O
ATOM	3694	C	TYR	388	50.563	60.288	30.714	1.00	41.88	AAAA C
ATOM	3695	O	TYR	388	50.727	59.092	30.511	1.00	32.99	AAAA O
ATOM	3696	N	SER	389	50.020	60.917	31.763	1.00	45.42	AAAA N
ATOM	3698	CA	SER	389	49.591	60.131	32.931	1.00	50.13	AAAA C
ATOM	3699	CB	SER	389	49.798	60.894	34.261	1.00	45.57	AAAA C
ATOM	3700	OG	SER	389	51.185	60.899	34.504	1.00	51.11	AAAA O
ATOM	3702	C	SER	389	48.097	59.813	32.804	1.00	48.11	AAAA C
ATOM	3703	O	SER	389	47.686	58.792	33.336	1.00	49.25	AAAA O
ATOM	3704	N	PHE	390	47.321	60.685	32.196	1.00	42.56	AAAA N
ATOM	3706	CA	PHE	390	45.867	60.595	32.146	1.00	40.76	AAAA C
ATOM	3707	CB	PHE	390	45.241	61.581	33.139	1.00	44.80	AAAA C
ATOM	3708	CG	PHE	390	43.764	61.358	33.328	1.00	40.53	AAAA C
ATOM	3709	CD1	PHE	390	43.406	60.273	34.089	1.00	40.80	AAAA C
ATOM	3710	CD2	PHE	390	42.768	62.157	32.748	1.00	35.59	AAAA C
ATOM	3711	CE1	PHE	390	42.050	59.985	34.312	1.00	47.09	AAAA C
ATOM	3712	CE2	PHE	390	41.454	61.824	32.965	1.00	44.50	AAAA C
ATOM	3713	CZ	PHE	390	41.063	60.745	33.739	1.00	34.54	AAAA C
ATOM	3714	C	PHE	390	45.372	60.829	30.720	1.00	38.54	AAAA C
ATOM	3715	O	PHE	390	45.542	61.918	30.126	1.00	40.29	AAAA O
ATOM	3716	N	TYR	391	44.819	59.818	30.096	1.00	33.48	AAAA N
ATOM	3718	CA	TYR	391	44.596	59.782	28.663	1.00	38.58	AAAA C
ATOM	3719	CB	TYR	391	45.579	58.871	27.972	1.00	38.95	AAAA C
ATOM	3720	CG	TYR	391	45.760	59.006	26.503	1.00	44.54	AAAA C
ATOM	3721	CD1	TYR	391	46.822	59.815	26.052	1.00	47.14	AAAA C
ATOM	3722	CE1	TYR	391	47.057	59.993	24.722	1.00	46.03	AAAA C
ATOM	3723	CD2	TYR	391	44.927	58.390	25.584	1.00	46.94	AAAA C
ATOM	3724	CE2	TYR	391	45.157	58.560	24.242	1.00	47.45	AAAA C
ATOM	3725	CZ	TYR	391	46.207	59.350	23.830	1.00	45.84	AAAA C

ATOM	3726	OH	TYR	391	46.374	59.492	22.481	1.00	44.70	AAAA O
ATOM	3728	C	TYR	391	43.194	59.232	28.349	1.00	39.74	AAAA C
ATOM	3729	O	TYR	391	42.841	58.103	28.736	1.00	38.49	AAAA O
ATOM	3730	N	VAL	392	42.417	60.158	27.779	1.00	37.97	AAAA N
ATOM	3732	CA	VAL	392	40.958	59.874	27.603	1.00	39.52	AAAA C
ATOM	3733	CB	VAL	392	40.075	60.880	28.440	1.00	41.12	AAAA C
ATOM	3734	CG1	VAL	392	38.612	60.464	28.472	1.00	37.96	AAAA C
ATOM	3735	CG2	VAL	392	40.666	61.041	29.841	1.00	33.19	AAAA C
ATOM	3736	C	VAL	392	40.531	60.092	26.182	1.00	31.08	AAAA C
ATOM	3737	O	VAL	392	40.508	61.277	25.804	1.00	34.71	AAAA O
ATOM	3738	N	LEU	393	40.299	59.113	25.383	1.00	34.62	AAAA N
ATOM	3740	CA	LEU	393	39.948	59.259	23.977	1.00	38.12	AAAA C
ATOM	3741	CB	LEU	393	41.200	59.036	23.096	1.00	42.49	AAAA C
ATOM	3742	CG	LEU	393	41.023	58.649	21.586	1.00	26.48	AAAA C
ATOM	3743	CD1	LEU	393	41.128	59.879	20.753	1.00	26.57	AAAA C
ATOM	3744	CD2	LEU	393	42.078	57.589	21.244	1.00	29.98	AAAA C
ATOM	3745	C	LEU	393	38.821	58.375	23.492	1.00	39.15	AAAA C
ATOM	3746	O	LEU	393	38.760	57.173	23.799	1.00	37.90	AAAA O
ATOM	3747	N	ASP	394	38.015	58.973	22.565	1.00	43.38	AAAA N
ATOM	3749	CA	ASP	394	36.888	58.215	21.975	1.00	44.77	AAAA C
ATOM	3750	CB	ASP	394	37.445	57.073	21.120	1.00	44.80	AAAA C
ATOM	3751	CG	ASP	394	36.466	56.477	20.156	1.00	47.14	AAAA C
ATOM	3752	OD1	ASP	394	36.750	55.577	19.333	1.00	52.91	AAAA O
ATOM	3753	OD2	ASP	394	35.311	56.948	20.180	1.00	49.27	AAAA O
ATOM	3754	C	ASP	394	35.936	57.619	23.021	1.00	43.17	AAAA C
ATOM	3755	O	ASP	394	35.831	56.385	23.212	1.00	43.51	AAAA O
ATOM	3756	N	ASN	395	35.299	58.495	23.746	1.00	39.90	AAAA N
ATOM	3758	CA	ASN	395	34.305	58.158	24.776	1.00	46.32	AAAA C
ATOM	3759	CB	ASN	395	34.804	58.512	26.212	1.00	42.96	AAAA C
ATOM	3760	CG	ASN	395	35.992	57.619	26.579	1.00	36.92	AAAA C
ATOM	3761	OD1	ASN	395	36.013	56.394	26.796	1.00	21.65	AAAA O
ATOM	3762	ND2	ASN	395	37.075	58.409	26.559	1.00	27.87	AAAA N
ATOM	3765	C	ASN	395	32.932	58.816	24.541	1.00	40.44	AAAA C
ATOM	3766	O	ASN	395	32.749	59.982	24.882	1.00	37.06	AAAA O
ATOM	3767	N	GLN	396	32.073	58.055	23.877	1.00	46.74	AAAA N
ATOM	3769	CA	GLN	396	30.771	58.582	23.421	1.00	52.93	AAAA C
ATOM	3770	CB	GLN	396	29.848	57.567	22.744	1.00	52.29	AAAA C
ATOM	3771	CG	GLN	396	30.173	57.405	21.257	1.00	46.42	AAAA C
ATOM	3772	CD	GLN	396	29.817	55.991	20.840	1.00	55.21	AAAA C
ATOM	3773	OE1	GLN	396	28.835	55.421	21.312	1.00	61.17	AAAA O
ATOM	3774	NE2	GLN	396	30.628	55.411	19.971	1.00	55.79	AAAA N
ATOM	3777	C	GLN	396	29.874	59.224	24.458	1.00	48.64	AAAA C
ATOM	3778	O	GLN	396	29.407	60.287	24.113	1.00	51.63	AAAA O
ATOM	3779	N	ASN	397	29.717	58.681	25.633	1.00	48.95	AAAA N
ATOM	3781	CA	ASN	397	28.783	59.196	26.632	1.00	51.72	AAAA C
ATOM	3782	CB	ASN	397	27.969	57.959	27.093	1.00	35.94	AAAA C
ATOM	3783	CG	ASN	397	27.231	57.430	25.860	1.00	49.09	AAAA C
ATOM	3784	OD1	ASN	397	26.591	58.304	25.229	1.00	49.32	AAAA O
ATOM	3785	ND2	ASN	397	27.258	56.175	25.431	1.00	43.31	AAAA N
ATOM	3788	C	ASN	397	29.367	59.945	27.800	1.00	52.98	AAAA C
ATOM	3789	O	ASN	397	28.586	60.344	28.627	1.00	53.33	AAAA O
ATOM	3790	N	LEU	398	30.682	59.990	28.001	1.00	55.73	AAAA N
ATOM	3792	CA	LEU	398	31.312	60.550	29.179	1.00	52.12	AAAA C
ATOM	3793	CB	LEU	398	32.927	60.388	29.149	1.00	48.47	AAAA C
ATOM	3794	CG	LEU	398	33.606	60.283	30.460	1.00	41.81	AAAA C
ATOM	3795	CD1	LEU	398	33.417	58.939	31.136	1.00	40.35	AAAA C
ATOM	3796	CD2	LEU	398	35.070	60.608	30.082	1.00	39.03	AAAA C
ATOM	3797	C	LEU	398	30.923	61.995	29.353	1.00	52.35	AAAA C
ATOM	3798	O	LEU	398	31.422	62.909	28.681	1.00	49.91	AAAA O
ATOM	3799	N	GLN	399	30.241	62.225	30.469	1.00	58.76	AAAA N
ATOM	3801	CA	GLN	399	29.688	63.558	30.796	1.00	60.93	AAAA C
ATOM	3802	CB	GLN	399	28.236	63.331	31.262	1.00	59.55	AAAA C
ATOM	3803	CG	GLN	399	27.235	63.962	30.316	1.00	73.07	AAAA C
ATOM	3804	CD	GLN	399	25.944	63.146	30.340	1.00	78.39	AAAA C
ATOM	3805	OE1	GLN	399	25.097	63.455	31.194	1.00	71.79	AAAA O
ATOM	3806	NE2	GLN	399	25.856	62.158	29.440	1.00	69.88	AAAA N
ATOM	3809	C	GLN	399	30.490	64.252	31.888	1.00	54.49	AAAA C
ATOM	3810	O	GLN	399	30.528	65.477	32.068	1.00	51.96	AAAA O
ATOM	3811	N	GLN	400	31.058	63.389	32.734	1.00	50.44	AAAA N
ATOM	3813	CA	GLN	400	31.938	63.948	33.756	1.00	53.83	AAAA C
ATOM	3814	CB	GLN	400	31.215	64.314	35.049	1.00	54.97	AAAA C
ATOM	3815	CG	GLN	400	30.717	63.150	35.897	1.00	58.99	AAAA C
ATOM	3816	CD	GLN	400	30.678	63.430	37.389	1.00	65.82	AAAA C
ATOM	3817	OE1	GLN	400	30.906	64.582	37.962	1.00	68.10	AAAA O
ATOM	3818	NE2	GLN	400	30.341	62.444	38.222	1.00	55.35	AAAA N
ATOM	3821	C	GLN	400	33.113	63.008	34.052	1.00	52.08	AAAA C
ATOM	3822	O	GLN	400	33.107	61.783	33.942	1.00	51.90	AAAA O
ATOM	3823	N	LEU	401	34.073	63.580	34.751	1.00	49.58	AAAA N
ATOM	3825	CA	LEU	401	35.175	62.844	35.334	1.00	49.57	AAAA C
ATOM	3826	CB	LEU	401	36.378	63.803	35.260	1.00	47.94	AAAA C
ATOM	3827	CG	LEU	401	36.636	64.237	33.772	1.00	46.61	AAAA C
ATOM	3828	CD1	LEU	401	37.658	65.326	33.677	1.00	39.09	AAAA C
ATOM	3829	CD2	LEU	401	36.919	63.062	32.860	1.00	40.72	AAAA C
ATOM	3830	C	LEU	401	34.866	62.357	36.734	1.00	51.23	AAAA C
ATOM	3831	O	LEU	401	34.258	61.299	36.892	1.00	49.06	AAAA O

ATOM	3832	N	TRP	402	35.297	63.140	37.690	1.00	54.58	AAAA N
ATOM	3834	CA	TRP	402	34.975	63.090	39.097	1.00	59.76	AAAA C
ATOM	3835	CB	TRP	402	36.279	62.953	39.933	1.00	59.56	AAAA C
ATOM	3836	CG	TRP	402	36.971	61.624	39.737	1.00	58.17	AAAA C
ATOM	3837	CD2	TRP	402	37.981	61.243	38.784	1.00	53.18	AAAA C
ATOM	3838	CE2	TRP	402	38.286	59.897	39.002	1.00	56.61	AAAA C
ATOM	3839	CE3	TRP	402	38.643	61.917	37.764	1.00	43.25	AAAA C
ATOM	3840	CD1	TRP	402	36.719	60.517	40.459	1.00	53.50	AAAA C
ATOM	3841	NE1	TRP	402	37.488	59.467	40.032	1.00	57.66	AAAA N
ATOM	3843	CZ2	TRP	402	39.212	59.160	38.249	1.00	51.44	AAAA C
ATOM	3844	CZ3	TRP	402	39.546	61.199	37.026	1.00	53.69	AAAA C
ATOM	3845	CH2	TRP	402	39.820	59.857	37.263	1.00	50.75	AAAA C
ATOM	3846	C	TRP	402	34.223	64.389	39.429	1.00	64.09	AAAA C
ATOM	3847	O	TRP	402	34.408	65.449	38.808	1.00	61.98	AAAA O
ATOM	3848	N	ASP	403	33.503	64.418	40.551	1.00	68.85	AAAA N
ATOM	3850	CA	ASP	403	32.947	65.668	41.068	1.00	67.83	AAAA C
ATOM	3851	CB	ASP	403	31.918	65.343	42.151	1.00	72.19	AAAA C
ATOM	3852	CG	ASP	403	30.853	66.417	42.306	1.00	73.08	AAAA C
ATOM	3853	OD1	ASP	403	31.177	67.625	42.297	1.00	71.67	AAAA O
ATOM	3854	OD2	ASP	403	29.693	65.979	42.454	1.00	75.08	AAAA O
ATOM	3855	C	ASP	403	34.005	66.607	41.607	1.00	66.63	AAAA C
ATOM	3856	O	ASP	403	34.245	66.672	42.811	1.00	67.18	AAAA O
ATOM	3857	N	TRP	404	34.449	67.588	40.846	1.00	69.29	AAAA N
ATOM	3859	CA	TRP	404	35.412	68.588	41.291	1.00	77.11	AAAA C
ATOM	3860	CB	TRP	404	35.859	69.409	40.063	1.00	79.10	AAAA C
ATOM	3861	CG	TRP	404	36.504	68.509	39.047	1.00	82.59	AAAA C
ATOM	3862	CD2	TRP	404	37.294	67.346	39.322	1.00	84.82	AAAA C
ATOM	3863	CE2	TRP	404	37.686	66.813	38.081	1.00	84.56	AAAA C
ATOM	3864	CE3	TRP	404	37.703	66.710	40.506	1.00	80.95	AAAA C
ATOM	3865	CD1	TRP	404	36.460	68.622	37.694	1.00	83.37	AAAA C
ATOM	3866	NE1	TRP	404	37.165	67.617	37.111	1.00	80.33	AAAA N
ATOM	3868	CZ2	TRP	404	38.477	65.662	37.982	1.00	85.91	AAAA C
ATOM	3869	CZ3	TRP	404	38.471	65.573	40.392	1.00	86.36	AAAA C
ATOM	3870	CH2	TRP	404	38.860	65.051	39.133	1.00	85.05	AAAA C
ATOM	3871	C	TRP	404	35.034	69.517	42.420	1.00	81.60	AAAA C
ATOM	3872	O	TRP	404	35.387	70.709	42.504	1.00	84.57	AAAA O
ATOM	3873	N	ASP	405	34.281	69.063	43.393	1.00	84.45	AAAA N
ATOM	3875	CA	ASP	405	33.771	69.861	44.496	1.00	87.48	AAAA C
ATOM	3876	CB	ASP	405	32.352	70.365	44.262	1.00	88.04	AAAA C
ATOM	3877	CG	ASP	405	32.274	71.612	43.409	1.00	92.54	AAAA C
ATOM	3878	OD1	ASP	405	33.306	72.285	43.207	1.00	94.82	AAAA O
ATOM	3879	OD2	ASP	405	31.130	71.854	42.955	1.00	95.26	AAAA O
ATOM	3880	C	ASP	405	33.730	68.906	45.693	1.00	87.80	AAAA C
ATOM	3881	O	ASP	405	34.245	69.224	46.743	1.00	92.18	AAAA O
ATOM	3882	N	ALA	406	33.239	67.709	45.460	1.00	84.46	AAAA N
ATOM	3884	CA	ALA	406	33.176	66.671	46.451	1.00	82.87	AAAA C
ATOM	3885	CB	ALA	406	31.943	65.805	46.133	1.00	76.32	AAAA C
ATOM	3886	C	ALA	406	34.445	65.840	46.459	1.00	85.77	AAAA C
ATOM	3887	O	ALA	406	34.470	64.823	47.185	1.00	89.38	AAAA O
ATOM	3888	N	ARG	407	35.433	66.073	45.577	1.00	83.74	AAAA N
ATOM	3890	CA	ARG	407	36.541	65.151	45.400	1.00	79.60	AAAA C
ATOM	3891	CB	ARG	407	36.165	64.140	44.297	1.00	77.84	AAAA C
ATOM	3892	CG	ARG	407	35.457	62.950	44.921	1.00	81.91	AAAA C
ATOM	3893	CD	ARG	407	35.362	61.688	44.113	1.00	86.97	AAAA C
ATOM	3894	NE	ARG	407	36.281	60.660	44.607	1.00	86.94	AAAA N
ATOM	3896	CZ	ARG	407	37.564	60.583	44.279	1.00	92.14	AAAA C
ATOM	3897	NH1	ARG	407	38.169	61.441	43.469	1.00	97.06	AAAA N
ATOM	3900	NH2	ARG	407	38.309	59.616	44.770	1.00	96.33	AAAA N
ATOM	3903	C	ARG	407	37.880	65.749	45.048	1.00	76.72	AAAA C
ATOM	3904	O	ARG	407	37.989	66.774	44.410	1.00	77.47	AAAA O
ATOM	3905	N	ASN	408	38.958	65.081	45.453	1.00	75.75	AAAA N
ATOM	3907	CA	ASN	408	40.311	65.556	45.173	1.00	73.79	AAAA C
ATOM	3908	CB	ASN	408	40.938	66.240	46.388	1.00	74.46	AAAA C
ATOM	3909	CG	ASN	408	41.986	67.242	45.947	1.00	82.51	AAAA C
ATOM	3910	OD1	ASN	408	41.813	68.429	46.240	1.00	90.33	AAAA O
ATOM	3911	ND2	ASN	408	43.028	66.821	45.253	1.00	84.46	AAAA N
ATOM	3914	C	ASN	408	41.257	64.468	44.654	1.00	65.97	AAAA C
ATOM	3915	O	ASN	408	41.251	63.374	45.151	1.00	63.82	AAAA O
ATOM	3916	N	LEU	409	42.041	64.793	43.650	1.00	61.41	AAAA N
ATOM	3918	CA	LEU	409	42.896	63.872	42.947	1.00	60.90	AAAA C
ATOM	3919	CB	LEU	409	42.153	63.250	41.768	1.00	62.98	AAAA C
ATOM	3920	CG	LEU	409	42.992	62.553	40.704	1.00	59.77	AAAA C
ATOM	3921	CD1	LEU	409	43.488	61.205	41.197	1.00	54.06	AAAA C
ATOM	3922	CD2	LEU	409	42.094	62.445	39.486	1.00	55.74	AAAA C
ATOM	3923	C	LEU	409	44.151	64.599	42.485	1.00	61.19	AAAA C
ATOM	3924	O	LEU	409	44.141	65.809	42.370	1.00	60.64	AAAA O
ATOM	3925	N	THR	410	45.281	63.903	42.424	1.00	63.74	AAAA N
ATOM	3927	CA	THR	410	46.588	64.462	42.131	1.00	60.44	AAAA C
ATOM	3928	CB	THR	410	47.454	64.676	43.385	1.00	67.08	AAAA C
ATOM	3929	OG1	THR	410	46.870	65.746	44.157	1.00	74.29	AAAA O
ATOM	3931	CG2	THR	410	48.909	65.103	43.162	1.00	48.56	AAAA C
ATOM	3932	C	THR	410	47.426	63.565	41.218	1.00	56.62	AAAA C
ATOM	3933	O	THR	410	47.382	62.354	41.317	1.00	54.99	AAAA O
ATOM	3934	N	ILE	411	48.077	64.245	40.288	1.00	53.97	AAAA N
ATOM	3936	CA	ILE	411	48.897	63.562	39.291	1.00	53.29	AAAA C

ATOM	3937	CB	ILE	411	48.409	63.854	37.864	1.00	49.81	AAAA C
ATOM	3938	CG2	ILE	411	49.216	63.128	36.806	1.00	30.86	AAAA C
ATOM	3939	CG1	ILE	411	46.911	63.489	37.729	1.00	40.83	AAAA C
ATOM	3940	CD1	ILE	411	46.322	63.547	36.338	1.00	38.51	AAAA C
ATOM	3941	C	ILE	411	50.319	64.018	39.568	1.00	55.38	AAAA C
ATOM	3942	O	ILE	411	50.656	65.179	39.291	1.00	57.59	AAAA O
ATOM	3943	N	SER	412	51.073	63.182	40.270	1.00	54.26	AAAA N
ATOM	3945	CA	SER	412	52.434	63.502	40.689	1.00	54.46	AAAA C
ATOM	3946	CB	SER	412	53.071	62.210	41.248	1.00	55.78	AAAA C
ATOM	3947	OG	SER	412	53.756	62.536	42.434	1.00	67.12	AAAA O
ATOM	3949	C	SER	412	53.326	63.910	39.523	1.00	55.52	AAAA C
ATOM	3950	O	SER	412	54.081	64.876	39.527	1.00	55.04	AAAA O
ATOM	3951	N	ALA	413	53.254	63.124	38.438	1.00	50.12	AAAA N
ATOM	3953	CA	ALA	413	54.064	63.402	37.281	1.00	50.01	AAAA C
ATOM	3954	CB	ALA	413	55.334	62.520	37.365	1.00	34.96	AAAA C
ATOM	3955	C	ALA	413	53.301	63.078	35.994	1.00	48.71	AAAA C
ATOM	3956	O	ALA	413	52.495	62.168	35.998	1.00	48.81	AAAA O
ATOM	3957	N	GLY	414	53.675	63.690	34.895	1.00	47.92	AAAA N
ATOM	3959	CA	GLY	414	53.057	63.454	33.607	1.00	51.75	AAAA C
ATOM	3960	C	GLY	414	52.017	64.524	33.294	1.00	52.77	AAAA C
ATOM	3961	O	GLY	414	51.684	65.370	34.114	1.00	53.23	AAAA O
ATOM	3962	N	LYS	415	51.385	64.406	32.138	1.00	56.31	AAAA N
ATOM	3964	CA	LYS	415	50.289	65.317	31.759	1.00	52.49	AAAA C
ATOM	3965	CB	LYS	415	50.884	66.358	30.833	1.00	50.94	AAAA C
ATOM	3966	CG	LYS	415	51.198	65.855	29.429	1.00	54.39	AAAA C
ATOM	3967	CD	LYS	415	52.288	66.691	28.765	1.00	53.96	AAAA C
ATOM	3968	CE	LYS	415	52.785	66.151	27.441	1.00	56.01	AAAA C
ATOM	3969	NZ	LYS	415	52.426	67.032	26.284	1.00	66.36	AAAA N
ATOM	3973	C	LYS	415	49.110	64.576	31.155	1.00	50.04	AAAA C
ATOM	3974	O	LYS	415	49.077	63.337	31.036	1.00	49.77	AAAA O
ATOM	3975	N	MET	416	48.091	65.353	30.771	1.00	48.34	AAAA N
ATOM	3977	CA	MET	416	46.890	64.734	30.186	1.00	46.77	AAAA C
ATOM	3978	CB	MET	416	45.629	65.186	30.949	1.00	42.79	AAAA C
ATOM	3979	CG	MET	416	45.836	65.880	32.273	1.00	40.91	AAAA C
ATOM	3980	SD	MET	416	44.511	65.636	33.517	1.00	56.20	AAAA S
ATOM	3981	CE	MET	416	44.002	67.366	33.690	1.00	35.94	AAAA C
ATOM	3982	C	MET	416	46.623	65.064	28.728	1.00	40.40	AAAA C
ATOM	3983	O	MET	416	46.963	66.137	28.247	1.00	34.84	AAAA O
ATOM	3984	N	TYR	417	45.893	64.169	28.104	1.00	38.49	AAAA N
ATOM	3986	CA	TYR	417	45.355	64.387	26.765	1.00	39.50	AAAA C
ATOM	3987	CB	TYR	417	46.156	63.471	25.831	1.00	32.02	AAAA C
ATOM	3988	CG	TYR	417	45.583	63.430	24.428	1.00	39.48	AAAA C
ATOM	3989	CD1	TYR	417	45.730	64.501	23.511	1.00	39.29	AAAA C
ATOM	3990	CE1	TYR	417	45.196	64.429	22.253	1.00	34.56	AAAA C
ATOM	3991	CD2	TYR	417	44.884	62.321	24.005	1.00	36.81	AAAA C
ATOM	3992	CE2	TYR	417	44.379	62.241	22.722	1.00	38.80	AAAA C
ATOM	3993	CZ	TYR	417	44.535	63.292	21.873	1.00	44.20	AAAA C
ATOM	3994	OH	TYR	417	44.053	63.361	20.552	1.00	58.10	AAAA O
ATOM	3996	C	TYR	417	43.853	64.065	26.698	1.00	44.18	AAAA C
ATOM	3997	O	TYR	417	43.376	62.974	27.135	1.00	42.19	AAAA O
ATOM	3998	N	PHE	418	43.068	64.971	26.100	1.00	45.84	AAAA N
ATOM	4000	CA	PHE	418	41.644	64.701	25.910	1.00	45.67	AAAA C
ATOM	4001	CB	PHE	418	40.772	65.657	26.739	1.00	47.19	AAAA C
ATOM	4002	CG	PHE	418	40.675	65.264	28.177	1.00	43.44	AAAA C
ATOM	4003	CD1	PHE	418	41.552	65.685	29.132	1.00	38.43	AAAA C
ATOM	4004	CD2	PHE	418	39.638	64.417	28.544	1.00	51.21	AAAA C
ATOM	4005	CE1	PHE	418	41.402	65.291	30.440	1.00	46.44	AAAA C
ATOM	4006	CE2	PHE	418	39.486	64.023	29.845	1.00	46.63	AAAA C
ATOM	4007	CZ	PHE	418	40.358	64.454	30.801	1.00	44.68	AAAA C
ATOM	4008	C	PHE	418	41.251	64.730	24.440	1.00	44.64	AAAA C
ATOM	4009	O	PHE	418	41.375	65.762	23.812	1.00	47.60	AAAA O
ATOM	4010	N	ALA	419	40.554	63.713	23.936	1.00	43.06	AAAA N
ATOM	4012	CA	ALA	419	40.015	63.793	22.607	1.00	39.21	AAAA C
ATOM	4013	CB	ALA	419	41.090	63.562	21.555	1.00	30.88	AAAA C
ATOM	4014	C	ALA	419	38.837	62.846	22.366	1.00	41.77	AAAA C
ATOM	4015	O	ALA	419	38.871	61.628	22.557	1.00	36.08	AAAA O
ATOM	4016	N	PHE	420	37.829	63.398	21.618	1.00	40.41	AAAA N
ATOM	4018	CA	PHE	420	36.742	62.621	21.070	1.00	40.03	AAAA C
ATOM	4019	CB	PHE	420	37.157	61.430	20.180	1.00	45.54	AAAA C
ATOM	4020	CG	PHE	420	37.832	61.909	18.912	1.00	54.18	AAAA C
ATOM	4021	CD1	PHE	420	39.221	61.987	18.751	1.00	49.23	AAAA C
ATOM	4022	CD2	PHE	420	37.006	62.345	17.871	1.00	47.65	AAAA C
ATOM	4023	CE1	PHE	420	39.783	62.496	17.567	1.00	46.00	AAAA C
ATOM	4024	CE2	PHE	420	37.572	62.833	16.725	1.00	51.10	AAAA C
ATOM	4025	CZ	PHE	420	38.964	62.928	16.549	1.00	44.01	AAAA C
ATOM	4026	C	PHE	420	35.762	62.146	22.126	1.00	41.65	AAAA C
ATOM	4027	O	PHE	420	35.352	60.991	22.215	1.00	38.35	AAAA O
ATOM	4028	N	ASN	421	35.459	63.024	23.049	1.00	45.35	AAAA N
ATOM	4030	CA	ASN	421	34.477	62.960	24.112	1.00	46.86	AAAA C
ATOM	4031	CB	ASN	421	35.183	63.276	25.449	1.00	43.60	AAAA C
ATOM	4032	CG	ASN	421	36.407	62.401	25.654	1.00	47.90	AAAA C
ATOM	4033	OD1	ASN	421	36.426	61.147	25.714	1.00	44.83	AAAA O
ATOM	4034	ND2	ASN	421	37.541	63.101	25.732	1.00	37.46	AAAA N
ATOM	4037	C	ASN	421	33.432	64.069	23.835	1.00	47.83	AAAA C
ATOM	4038	O	ASN	421	33.617	65.233	24.237	1.00	38.95	AAAA O

ATOM	4039	N	PRO	422	32.453	63.777	22.968	1.00	47.86	AAAA N
ATOM	4040	CD	PRO	422	32.213	62.423	22.372	1.00	44.11	AAAA C
ATOM	4041	CA	PRO	422	31.463	64.776	22.605	1.00	47.85	AAAA C
ATOM	4042	CB	PRO	422	30.731	64.084	21.446	1.00	44.86	AAAA C
ATOM	4043	CG	PRO	422	30.947	62.623	21.606	1.00	43.01	AAAA C
ATOM	4044	C	PRO	422	30.577	65.284	23.735	1.00	51.16	AAAA C
ATOM	4045	O	PRO	422	30.223	66.486	23.744	1.00	48.54	AAAA O
ATOM	4046	N	LYS	423	30.320	64.487	24.774	1.00	52.90	AAAA N
ATOM	4048	CA	LYS	423	29.431	64.908	25.865	1.00	58.82	AAAA C
ATOM	4049	CB	LYS	423	28.556	63.721	26.360	1.00	52.93	AAAA C
ATOM	4050	CG	LYS	423	28.209	62.810	25.196	1.00	70.55	AAAA C
ATOM	4051	CD	LYS	423	26.743	62.448	24.996	1.00	73.79	AAAA C
ATOM	4052	CE	LYS	423	26.030	63.374	24.021	1.00	77.06	AAAA C
ATOM	4053	NZ	LYS	423	25.949	64.748	24.614	1.00	64.99	AAAA N
ATOM	4057	C	LYS	423	30.158	65.482	27.071	1.00	57.43	AAAA C
ATOM	4058	O	LYS	423	29.582	65.478	28.152	1.00	55.22	AAAA O
ATOM	4059	N	LEU	424	31.425	65.859	26.862	1.00	55.95	AAAA N
ATOM	4061	CA	LEU	424	32.261	66.162	28.017	1.00	57.07	AAAA C
ATOM	4062	CB	LEU	424	33.463	65.250	28.237	1.00	49.16	AAAA C
ATOM	4063	CG	LEU	424	34.390	65.748	29.370	1.00	68.27	AAAA C
ATOM	4064	CD1	LEU	424	33.821	65.362	30.734	1.00	60.66	AAAA C
ATOM	4065	CD2	LEU	424	35.825	65.276	29.123	1.00	60.35	AAAA C
ATOM	4066	C	LEU	424	32.709	67.585	27.878	1.00	56.29	AAAA C
ATOM	4067	O	LEU	424	33.696	67.861	27.201	1.00	59.98	AAAA O
ATOM	4068	N	CYS	425	31.995	68.488	28.492	1.00	58.76	AAAA N
ATOM	4070	CA	CYS	425	32.342	69.916	28.406	1.00	60.39	AAAA C
ATOM	4071	C	CYS	425	33.771	70.119	28.810	1.00	62.59	AAAA C
ATOM	4072	O	CYS	425	34.288	69.665	29.831	1.00	64.45	AAAA O
ATOM	4073	CB	CYS	425	31.249	70.644	29.214	1.00	68.23	AAAA C
ATOM	4074	SG	CYS	425	29.916	71.303	28.086	1.00	81.03	AAAA S
ATOM	4075	N	VAL	426	34.529	70.953	28.102	1.00	65.31	AAAA N
ATOM	4077	CA	VAL	426	35.943	71.149	28.358	1.00	65.49	AAAA C
ATOM	4078	CB	VAL	426	36.644	72.022	27.310	1.00	66.66	AAAA C
ATOM	4079	CG1	VAL	426	36.715	71.413	25.925	1.00	62.49	AAAA C
ATOM	4080	CG2	VAL	426	35.962	73.365	27.239	1.00	60.92	AAAA C
ATOM	4081	C	VAL	426	36.105	71.711	29.757	1.00	65.99	AAAA C
ATOM	4082	O	VAL	426	37.180	71.724	30.388	1.00	64.51	AAAA O
ATOM	4083	N	SER	427	35.090	72.361	30.267	1.00	67.67	AAAA N
ATOM	4085	CA	SER	427	35.091	72.927	31.599	1.00	66.85	AAAA C
ATOM	4086	CB	SER	427	33.685	73.499	31.864	1.00	61.16	AAAA C
ATOM	4087	OG	SER	427	34.088	74.860	32.098	1.00	67.05	AAAA O
ATOM	4089	C	SER	427	35.515	71.972	32.701	1.00	64.24	AAAA C
ATOM	4090	O	SER	427	36.332	72.328	33.573	1.00	63.66	AAAA O
ATOM	4091	N	GLU	428	34.965	70.771	32.618	1.00	58.75	AAAA N
ATOM	4093	CA	GLU	428	35.384	69.753	33.585	1.00	63.39	AAAA C
ATOM	4094	CB	GLU	428	34.594	68.485	33.240	1.00	68.67	AAAA C
ATOM	4095	CG	GLU	428	33.115	68.560	33.537	1.00	66.59	AAAA C
ATOM	4096	CD	GLU	428	32.785	68.560	35.023	1.00	72.33	AAAA C
ATOM	4097	OE1	GLU	428	32.729	67.522	35.722	1.00	81.62	AAAA O
ATOM	4098	OE2	GLU	428	32.581	69.688	35.517	1.00	70.97	AAAA O
ATOM	4099	C	GLU	428	36.870	69.485	33.429	1.00	61.63	AAAA C
ATOM	4100	O	GLU	428	37.671	69.696	34.307	1.00	62.03	AAAA O
ATOM	4101	N	ILE	429	37.265	69.262	32.165	1.00	61.26	AAAA N
ATOM	4103	CA	ILE	429	38.631	69.038	31.789	1.00	61.09	AAAA C
ATOM	4104	CB	ILE	429	38.759	68.933	30.263	1.00	59.32	AAAA C
ATOM	4105	CG2	ILE	429	40.257	68.915	29.895	1.00	45.93	AAAA C
ATOM	4106	CG1	ILE	429	37.968	67.719	29.794	1.00	57.66	AAAA C
ATOM	4107	CD1	ILE	429	38.038	67.555	28.285	1.00	53.48	AAAA C
ATOM	4108	C	ILE	429	39.498	70.166	32.323	1.00	61.90	AAAA C
ATOM	4109	O	ILE	429	40.592	70.017	32.867	1.00	61.28	AAAA O
ATOM	4110	N	TYR	430	38.987	71.384	32.200	1.00	65.34	AAAA N
ATOM	4112	CA	TYR	430	39.729	72.543	32.719	1.00	68.10	AAAA C
ATOM	4113	CB	TYR	430	39.180	73.822	32.099	1.00	71.02	AAAA C
ATOM	4114	CG	TYR	430	39.538	74.006	30.639	1.00	75.98	AAAA C
ATOM	4115	CD1	TYR	430	38.653	73.821	29.599	1.00	77.60	AAAA C
ATOM	4116	CE1	TYR	430	38.953	73.977	28.270	1.00	75.72	AAAA C
ATOM	4117	CD2	TYR	430	40.810	74.401	30.260	1.00	75.95	AAAA C
ATOM	4118	CE2	TYR	430	41.155	74.575	28.937	1.00	74.81	AAAA C
ATOM	4119	CZ	TYR	430	40.221	74.359	27.952	1.00	78.51	AAAA C
ATOM	4120	OH	TYR	430	40.564	74.542	26.616	1.00	85.40	AAAA O
ATOM	4122	C	TYR	430	39.779	72.634	34.241	1.00	63.72	AAAA C
ATOM	4123	O	TYR	430	40.654	73.321	34.758	1.00	58.26	AAAA O
ATOM	4124	N	ARG	431	38.819	72.017	34.907	1.00	65.53	AAAA N
ATOM	4126	CA	ARG	431	38.747	72.043	36.356	1.00	68.15	AAAA C
ATOM	4127	CB	ARG	431	37.348	71.748	36.898	1.00	73.32	AAAA C
ATOM	4128	CG	ARG	431	37.345	71.815	38.430	1.00	82.99	AAAA C
ATOM	4129	CD	ARG	431	37.270	73.279	38.860	1.00	88.39	AAAA C
ATOM	4130	NE	ARG	431	37.698	73.472	40.258	1.00	92.48	AAAA N
ATOM	4132	CZ	ARG	431	36.835	73.258	41.259	1.00	94.93	AAAA C
ATOM	4133	NH1	ARG	431	35.610	72.872	40.872	1.00	87.40	AAAA N
ATOM	4136	NH2	ARG	431	37.021	73.371	42.567	1.00	95.17	AAAA N
ATOM	4139	C	ARG	431	39.718	70.986	36.877	1.00	67.75	AAAA C
ATOM	4140	O	ARG	431	40.637	71.292	37.629	1.00	66.74	AAAA O
ATOM	4141	N	MET	432	39.541	69.791	36.305	1.00	63.87	AAAA N
ATOM	4143	CA	MET	432	40.437	68.703	36.652	1.00	64.46	AAAA C

ATOM	4144	CB	MET	432	40.237	67.622	35.719	1.00	54.25	AAAA C
ATOM	4145	CG	MET	432	41.254	66.426	35.971	1.00	40.18	AAAA C
ATOM	4146	SD	MET	432	40.829	64.925	35.112	1.00	52.21	AAAA S
ATOM	4147	CE	MET	432	41.582	63.681	36.137	1.00	54.99	AAAA C
ATOM	4148	C	MET	432	41.891	69.170	36.626	1.00	64.65	AAAA C
ATOM	4149	O	MET	432	42.530	68.992	37.653	1.00	65.88	AAAA O
ATOM	4150	N	GLU	433	42.331	69.811	35.556	1.00	65.78	AAAA N
ATOM	4152	CA	GLU	433	43.622	70.469	35.510	1.00	69.16	AAAA C
ATOM	4153	CB	GLU	433	43.704	71.506	34.401	1.00	69.58	AAAA C
ATOM	4154	CG	GLU	433	44.121	70.967	33.048	1.00	76.91	AAAA C
ATOM	4155	CD	GLU	433	44.623	72.149	32.242	1.00	82.02	AAAA C
ATOM	4156	OE1	GLU	433	44.718	73.224	32.874	1.00	86.82	AAAA O
ATOM	4157	OE2	GLU	433	44.905	72.050	31.042	1.00	88.26	AAAA O
ATOM	4158	C	GLU	433	44.016	71.219	36.781	1.00	71.29	AAAA C
ATOM	4159	O	GLU	433	45.133	71.083	37.294	1.00	74.29	AAAA O
ATOM	4160	N	GLU	434	43.178	72.120	37.280	1.00	72.93	AAAA N
ATOM	4162	CA	GLU	434	43.505	72.873	38.485	1.00	72.88	AAAA C
ATOM	4163	CB	GLU	434	42.458	73.916	38.840	1.00	81.36	AAAA C
ATOM	4164	CG	GLU	434	41.191	73.956	38.032	1.00	83.34	AAAA C
ATOM	4165	CD	GLU	434	40.181	75.004	38.432	1.00	97.32	AAAA C
ATOM	4166	OE1	GLU	434	39.521	74.928	39.505	1.00	97.34	AAAA O
ATOM	4167	OE2	GLU	434	40.080	75.941	37.583	1.00	99.95	AAAA O
ATOM	4168	C	GLU	434	43.675	71.886	39.632	1.00	71.46	AAAA C
ATOM	4169	O	GLU	434	44.728	71.858	40.251	1.00	78.49	AAAA O
ATOM	4170	N	VAL	435	42.670	71.095	39.926	1.00	66.34	AAAA N
ATOM	4172	CA	VAL	435	42.711	70.129	41.001	1.00	62.49	AAAA C
ATOM	4173	CB	VAL	435	41.451	69.217	40.972	1.00	60.38	AAAA C
ATOM	4174	CG1	VAL	435	41.547	68.214	42.104	1.00	52.32	AAAA C
ATOM	4175	CG2	VAL	435	40.203	70.073	41.029	1.00	50.79	AAAA C
ATOM	4176	C	VAL	435	43.939	69.253	41.018	1.00	60.74	AAAA C
ATOM	4177	O	VAL	435	44.607	69.165	42.034	1.00	62.37	AAAA O
ATOM	4178	N	THR	436	44.282	68.506	39.988	1.00	60.67	AAAA N
ATOM	4180	CA	THR	436	45.335	67.516	39.936	1.00	56.36	AAAA C
ATOM	4181	CB	THR	436	45.199	66.565	38.736	1.00	50.92	AAAA C
ATOM	4182	OG1	THR	436	44.913	67.283	37.503	1.00	47.03	AAAA O
ATOM	4184	CG2	THR	436	44.108	65.526	38.901	1.00	54.38	AAAA C
ATOM	4185	C	THR	436	46.701	68.184	39.930	1.00	60.55	AAAA C
ATOM	4186	O	THR	436	47.714	67.490	40.024	1.00	60.61	AAAA O
ATOM	4187	N	GLY	437	46.836	69.496	39.835	1.00	60.65	AAAA N
ATOM	4189	CA	GLY	437	48.102	70.164	39.749	1.00	59.47	AAAA C
ATOM	4190	C	GLY	437	48.800	69.864	38.424	1.00	64.78	AAAA C
ATOM	4191	O	GLY	437	49.983	70.254	38.245	1.00	62.70	AAAA O
ATOM	4192	N	THR	438	48.112	69.387	37.380	1.00	63.79	AAAA N
ATOM	4194	CA	THR	438	48.731	69.169	36.076	1.00	65.09	AAAA C
ATOM	4195	CB	THR	438	47.967	68.027	35.411	1.00	66.87	AAAA C
ATOM	4196	OG1	THR	438	46.600	68.385	35.731	1.00	62.22	AAAA O
ATOM	4198	CG2	THR	438	48.208	66.659	36.019	1.00	68.74	AAAA C
ATOM	4199	C	THR	438	48.590	70.415	35.220	1.00	66.14	AAAA C
ATOM	4200	O	THR	438	49.003	70.543	34.070	1.00	68.05	AAAA O
ATOM	4201	N	LYS	439	48.089	71.481	35.822	1.00	67.37	AAAA N
ATOM	4203	CA	LYS	439	47.927	72.757	35.154	1.00	71.08	AAAA C
ATOM	4204	CB	LYS	439	47.114	73.708	36.034	1.00	69.23	AAAA C
ATOM	4205	CG	LYS	439	46.677	74.938	35.265	1.00	77.26	AAAA C
ATOM	4206	CD	LYS	439	45.832	75.942	36.014	1.00	81.65	AAAA C
ATOM	4207	CE	LYS	439	44.385	75.475	36.182	1.00	87.39	AAAA C
ATOM	4208	NZ	LYS	439	43.667	76.431	37.100	1.00	93.85	AAAA N
ATOM	4212	C	LYS	439	49.249	73.396	34.752	1.00	73.01	AAAA C
ATOM	4213	O	LYS	439	49.996	73.986	35.541	1.00	74.60	AAAA O
ATOM	4214	N	GLY	440	49.517	73.453	33.441	1.00	73.33	AAAA N
ATOM	4216	CA	GLY	440	50.733	74.167	33.014	1.00	71.39	AAAA C
ATOM	4217	C	GLY	440	51.716	73.204	32.389	1.00	71.20	AAAA C
ATOM	4218	O	GLY	440	52.684	73.650	31.822	1.00	72.70	AAAA O
ATOM	4219	N	ARG	441	51.445	71.908	32.436	1.00	72.99	AAAA N
ATOM	4221	CA	ARG	441	52.343	70.945	31.831	1.00	74.12	AAAA C
ATOM	4222	CB	ARG	441	52.617	69.740	32.716	1.00	69.44	AAAA C
ATOM	4223	CG	ARG	441	51.847	69.695	34.003	1.00	63.34	AAAA C
ATOM	4224	CD	ARG	441	52.060	68.314	34.595	1.00	67.64	AAAA C
ATOM	4225	NE	ARG	441	52.244	68.395	36.030	1.00	61.00	AAAA N
ATOM	4227	CZ	ARG	441	52.326	67.357	36.831	1.00	59.21	AAAA C
ATOM	4228	NH1	ARG	441	52.258	66.117	36.395	1.00	60.57	AAAA N
ATOM	4231	NH2	ARG	441	52.468	67.596	38.128	1.00	72.94	AAAA N
ATOM	4234	C	ARG	441	51.760	70.446	30.511	1.00	73.50	AAAA C
ATOM	4235	O	ARG	441	52.195	69.424	30.012	1.00	74.73	AAAA O
ATOM	4236	N	GLN	442	50.732	71.114	30.043	1.00	74.69	AAAA N
ATOM	4238	CA	GLN	442	49.959	70.646	28.914	1.00	75.13	AAAA C
ATOM	4239	CB	GLN	442	48.457	70.875	29.126	1.00	68.73	AAAA C
ATOM	4240	CG	GLN	442	47.669	69.576	29.195	1.00	71.20	AAAA C
ATOM	4241	CD	GLN	442	47.623	69.028	30.607	1.00	70.98	AAAA C
ATOM	4242	OE1	GLN	442	47.714	67.822	30.868	1.00	78.66	AAAA O
ATOM	4243	NE2	GLN	442	47.477	69.907	31.584	1.00	66.86	AAAA N
ATOM	4246	C	GLN	442	50.326	71.359	27.627	1.00	77.69	AAAA C
ATOM	4247	O	GLN	442	50.227	72.569	27.530	1.00	75.57	AAAA O
ATOM	4248	N	ALA	443	50.474	70.554	26.575	1.00	81.54	AAAA N
ATOM	4250	CA	ALA	443	50.643	71.148	25.236	1.00	82.95	AAAA C
ATOM	4251	CB	ALA	443	51.104	70.118	24.220	1.00	81.69	AAAA C

ATOM	4352	C	ALA	443	49.259	71.706	24.952	1.00	83.73	AAAA C
ATOM	4353	O	ALA	443	48.398	71.744	25.830	1.00	83.87	AAAA O
ATOM	4354	N	LYS	444	48.914	72.052	23.713	1.00	86.20	AAAA N
ATOM	4356	CA	LYS	444	47.559	72.524	23.482	1.00	85.88	AAAA C
ATOM	4357	CB	LYS	444	47.426	73.997	23.128	1.00	83.99	AAAA C
ATOM	4358	CG	LYS	444	46.673	74.734	24.241	1.00	93.60	AAAA C
ATOM	4359	CD	LYS	444	45.883	73.841	25.186	1.00	95.14	AAAA C
ATOM	4360	CE	LYS	444	46.390	73.786	26.614	1.00	97.04	AAAA C
ATOM	4361	NZ	LYS	444	45.368	73.090	27.473	1.00	97.22	AAAA N
ATOM	4365	C	LYS	444	46.659	71.779	22.508	1.00	84.20	AAAA C
ATOM	4366	O	LYS	444	45.428	71.901	22.635	1.00	85.63	AAAA O
ATOM	4367	N	GLY	445	47.214	70.734	21.916	1.00	78.85	AAAA N
ATOM	4369	CA	GLY	445	46.368	69.786	21.208	1.00	75.06	AAAA C
ATOM	4370	C	GLY	445	45.803	68.844	22.260	1.00	72.30	AAAA C
ATOM	4371	O	GLY	445	44.963	67.993	21.940	1.00	74.90	AAAA O
ATOM	4372	N	ASP	446	46.300	68.981	23.492	1.00	67.97	AAAA N
ATOM	4374	CA	ASP	446	45.914	68.174	24.642	1.00	62.81	AAAA C
ATOM	4375	CB	ASP	446	46.754	68.552	25.873	1.00	55.24	AAAA C
ATOM	4376	CG	ASP	446	48.213	68.169	25.801	1.00	54.07	AAAA C
ATOM	4377	OD1	ASP	446	48.693	67.385	24.946	1.00	45.08	AAAA O
ATOM	4378	OD2	ASP	446	49.091	68.595	26.593	1.00	50.12	AAAA O
ATOM	4379	C	ASP	446	44.438	68.274	25.016	1.00	58.07	AAAA C
ATOM	4380	O	ASP	446	43.610	67.369	25.127	1.00	55.59	AAAA O
ATOM	4381	N	ILE	447	44.043	69.527	25.226	1.00	54.13	AAAA N
ATOM	4383	CA	ILE	447	42.652	69.822	25.510	1.00	54.09	AAAA C
ATOM	4384	CB	ILE	447	42.505	70.502	26.877	1.00	48.92	AAAA C
ATOM	4385	CG2	ILE	447	41.030	70.663	27.182	1.00	41.02	AAAA C
ATOM	4386	CG1	ILE	447	43.211	69.621	27.932	1.00	52.36	AAAA C
ATOM	4387	CD1	ILE	447	43.468	70.329	29.237	1.00	48.47	AAAA C
ATOM	4388	C	ILE	447	42.027	70.591	24.364	1.00	53.06	AAAA C
ATOM	4389	O	ILE	447	41.718	71.772	24.423	1.00	56.08	AAAA O
ATOM	4390	N	ASN	448	41.625	69.915	23.307	1.00	53.17	AAAA N
ATOM	4392	CA	ASN	448	41.013	70.642	22.202	1.00	54.61	AAAA C
ATOM	4393	CB	ASN	448	41.283	69.982	20.863	1.00	49.17	AAAA C
ATOM	4394	CG	ASN	448	40.415	68.786	20.577	1.00	49.40	AAAA C
ATOM	4395	OD1	ASN	448	39.287	68.977	20.113	1.00	52.34	AAAA O
ATOM	4396	ND2	ASN	448	40.990	67.622	20.871	1.00	52.49	AAAA N
ATOM	4399	C	ASN	448	39.518	70.824	22.402	1.00	56.44	AAAA C
ATOM	4400	O	ASN	448	38.816	69.974	22.939	1.00	55.83	AAAA O
ATOM	4401	N	THR	449	39.071	71.917	21.764	1.00	58.52	AAAA N
ATOM	4403	CA	THR	449	37.682	72.351	21.901	1.00	58.62	AAAA C
ATOM	4404	CB	THR	449	37.497	73.845	22.169	1.00	55.90	AAAA C
ATOM	4405	OG1	THR	449	37.913	74.485	20.943	1.00	68.89	AAAA O
ATOM	4407	CG2	THR	449	38.354	74.352	23.310	1.00	59.06	AAAA C
ATOM	4408	C	THR	449	36.920	72.053	20.628	1.00	56.82	AAAA C
ATOM	4409	O	THR	449	35.750	72.381	20.473	1.00	60.87	AAAA O
ATOM	4410	N	ARG	450	37.539	71.304	19.757	1.00	55.76	AAAA N
ATOM	4412	CA	ARG	450	36.887	70.935	18.507	1.00	54.66	AAAA C
ATOM	4413	CB	ARG	450	37.845	71.179	17.377	1.00	48.33	AAAA C
ATOM	4414	CG	ARG	450	38.385	69.975	16.645	1.00	54.81	AAAA C
ATOM	4415	CD	ARG	450	39.487	70.561	15.696	1.00	44.92	AAAA C
ATOM	4416	NE	ARG	450	40.706	70.719	16.488	1.00	52.49	AAAA N
ATOM	4418	CZ	ARG	450	41.544	69.757	16.882	1.00	39.08	AAAA C
ATOM	4419	NH1	ARG	450	41.176	68.572	16.466	1.00	41.07	AAAA N
ATOM	4422	NH2	ARG	450	42.601	70.001	17.610	1.00	45.18	AAAA N
ATOM	4425	C	ARG	450	36.267	69.553	18.557	1.00	56.82	AAAA C
ATOM	4426	O	ARG	450	35.186	69.303	17.992	1.00	58.15	AAAA O
ATOM	4427	N	ASN	451	36.800	68.583	19.324	1.00	56.66	AAAA N
ATOM	4429	CA	ASN	451	36.107	67.311	19.434	1.00	50.27	AAAA C
ATOM	4430	CB	ASN	451	36.725	66.127	18.760	1.00	48.54	AAAA C
ATOM	4431	CG	ASN	451	38.243	66.143	18.764	1.00	60.51	AAAA C
ATOM	4432	OD1	ASN	451	38.779	66.279	19.855	1.00	53.45	AAAA O
ATOM	4433	ND2	ASN	451	38.707	65.976	17.506	1.00	54.88	AAAA N
ATOM	4436	C	ASN	451	35.849	66.854	20.869	1.00	52.97	AAAA C
ATOM	4437	O	ASN	451	35.330	65.750	21.096	1.00	49.71	AAAA O
ATOM	4438	N	ASN	452	36.126	67.668	21.851	1.00	51.98	AAAA N
ATOM	4440	CA	ASN	452	35.769	67.485	23.229	1.00	55.88	AAAA C
ATOM	4441	CB	ASN	452	36.947	67.873	24.136	1.00	54.62	AAAA C
ATOM	4442	CG	ASN	452	37.936	66.736	24.285	1.00	60.96	AAAA C
ATOM	4443	OD1	ASN	452	37.646	65.633	24.735	1.00	51.30	AAAA O
ATOM	4444	ND2	ASN	452	39.153	67.098	23.855	1.00	56.75	AAAA N
ATOM	4447	C	ASN	452	34.603	68.385	23.688	1.00	58.11	AAAA C
ATOM	4448	O	ASN	452	34.785	69.629	23.657	1.00	55.07	AAAA O
ATOM	4449	N	GLY	453	33.444	67.813	23.985	1.00	55.08	AAAA N
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ATOM	4452	C	GLY	453	31.500	69.269	23.174	1.00	64.95	AAAA C
ATOM	4453	O	GLY	453	30.302	69.603	23.276	1.00	65.71	AAAA O
ATOM	4454	N	GLU	454	31.910	69.109	21.910	1.00	67.44	AAAA N
ATOM	4456	CA	GLU	454	31.266	69.543	20.690	1.00	63.63	AAAA C
ATOM	4457	CB	GLU	454	31.739	68.818	19.401	1.00	53.71	AAAA C
ATOM	4458	CG	GLU	454	32.349	67.430	19.738	1.00	49.50	AAAA C
ATOM	4459	CD	GLU	454	32.368	66.620	18.454	1.00	54.61	AAAA C
ATOM	4460	OE1	GLU	454	31.368	66.637	17.702	0.01	54.10	AAAA O
ATOM	4461	OE2	GLU	454	33.417	66.003	18.160	0.01	54.17	AAAA O
ATOM	4462	C	GLU	454	29.762	69.301	20.767	1.00	65.41	AAAA C

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ATOM	4366	CA	ARG	455	27.843	67.997	21.371	1.00 69.33	AAAA C
ATOM	4367	CB	ARG	455	27.448	66.733	20.652	1.00 73.38	AAAA C
ATOM	4368	CG	ARG	455	28.467	65.912	19.924	1.00 74.27	AAAA C
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ATOM	4370	NE	ARG	455	27.301	63.638	20.052	1.00 86.31	AAAA N
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ATOM	4376	NH2	ARG	455	27.225	61.523	21.003	1.00 87.36	AAAA N
ATOM	4379	C	ARG	455	27.213	67.934	22.756	1.00 67.35	AAAA C
ATOM	4380	O	ARG	455	26.423	67.025	22.961	1.00 66.26	AAAA O
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ATOM	4389	CA	SER	457	25.431	72.095	26.358	0.50 69.64	AAAA C
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ATOM	4391	OG	SER	457	23.422	73.294	26.060	0.50 73.31	AAAA O
ATOM	4393	C	SER	457	26.418	72.510	27.437	0.50 69.27	AAAA C
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ATOM	4407	OT	ALA	459	28.855	76.301	31.054	0.50 68.22	AAAA O
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ATOM	4550	C1	NAG	463	33.054	15.249	72.938	1.00 43.58	AAAA C
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ATOM	4620	C6	NAG	465	29.461	19.647	77.930	1.00 75.64	AAAA C

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ATOM   4623  O6  NAG   465      28.385  19.238  77.142  1.00 76.25      AAAA O
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ATOM   4413  N   ALA   479      40.696  74.461  14.624  1.00 86.43      BBBB N
ATOM   4415  CA  ALA   479      41.033  74.108  16.033  1.00 89.85      BBBB C
ATOM   4416  N   ALA   480      38.749  74.752  16.610  1.00 92.12      BBBB N
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ATOM   4420  C   ALA   480      36.306  75.030  16.849  1.00 91.39      BBBB C
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ATOM   4422  N   GLN   481      36.135  75.304  15.564  0.01 89.69      BBBB N
ATOM   4424  CA  GLN   481      34.832  75.164  14.915  1.00 87.19      BBBB C
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ATOM   4426  CG  GLN   481      34.277  77.627  15.220  1.00 99.93      BBBB C
ATOM   4427  CD  GLN   481      34.067  79.003  14.626  1.00103.59      BBBB C
ATOM   4428  OE1 GLN   481      35.011  79.777  14.381  1.00103.27      BBBB O
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ATOM   4439  CD  LYS   482      39.413  72.968  11.471  1.00 80.62      BBBB C
ATOM   4440  CE  LYS   482      39.985  74.310  11.027  0.01 76.66      BBBB C
ATOM   4441  NZ  LYS   482      41.252  74.136  10.262  0.01 76.20      BBBB N
ATOM   4445  C   LYS   482      35.779  70.701  13.872  1.00 67.70      BBBB C
ATOM   4446  O   LYS   482      35.879  70.744  15.092  1.00 69.99      BBBB O
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ATOM   4450  CB  LEU   483      34.256  67.529  13.039  1.00 55.20      BBBB C
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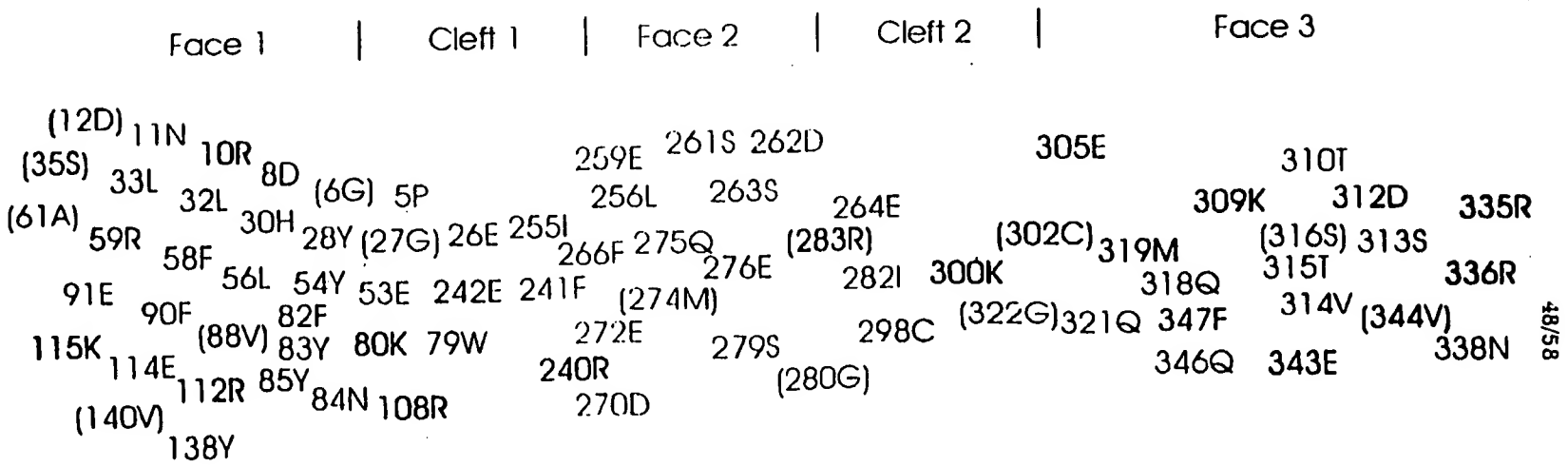
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Cleft 1
Face 2
Cleft 2
Face 3
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11N
10R
8D
(6G)
5P
(35S)
33L
32L
30H
28Y
(27G)
26E
(61A)
59R
58F
56L
54Y
53E
242E
241F
91E
90F
82F
115K
(88V)
83Y
80K
79W
114E
112R
85Y
84N
108R
(140V)
138Y
259E
261S
262D
256L
263S
264E
255I
266F
275Q
(283R)
276E
(274M)
282I
272E
279S
298C
240R
(280G)
270D
305E
310T
309K
312D
335R
(302C)
319M
(316S)
313S
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336R
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346Q
343E
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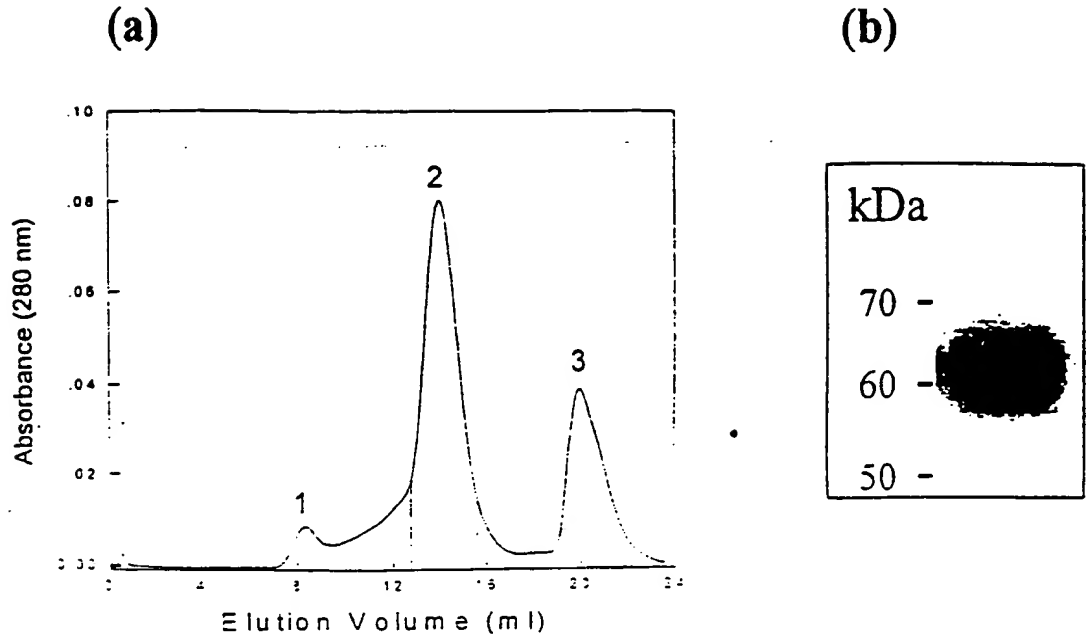
Figure 2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(b)
Absorbance (280 nm)
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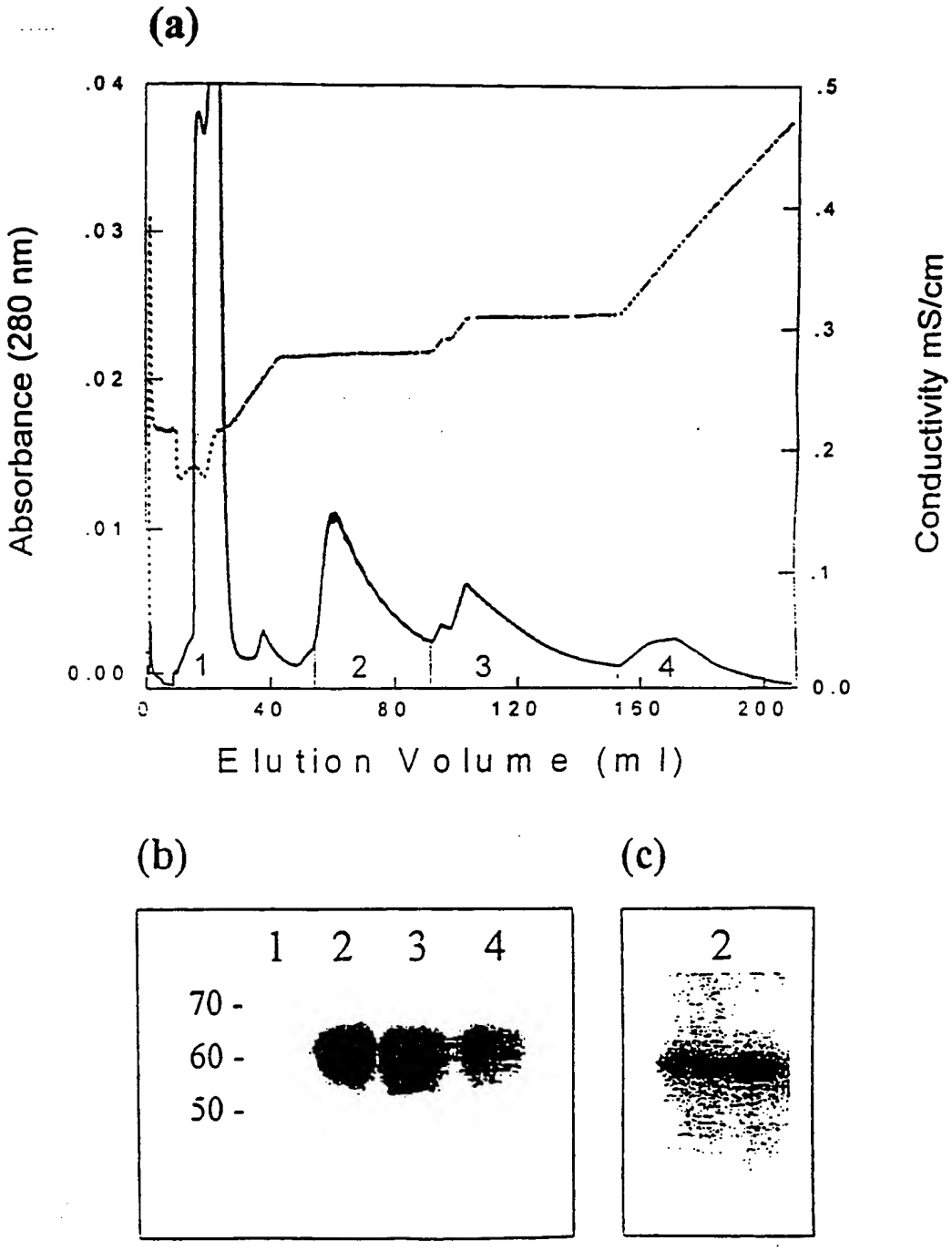
.08
.06
.04
.02
1
2
3
Elution Volume (ml)
kDa
70
60
50

Figure 3


(a)
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.03
.02
.01
0.00
Absorbance (280 nm)
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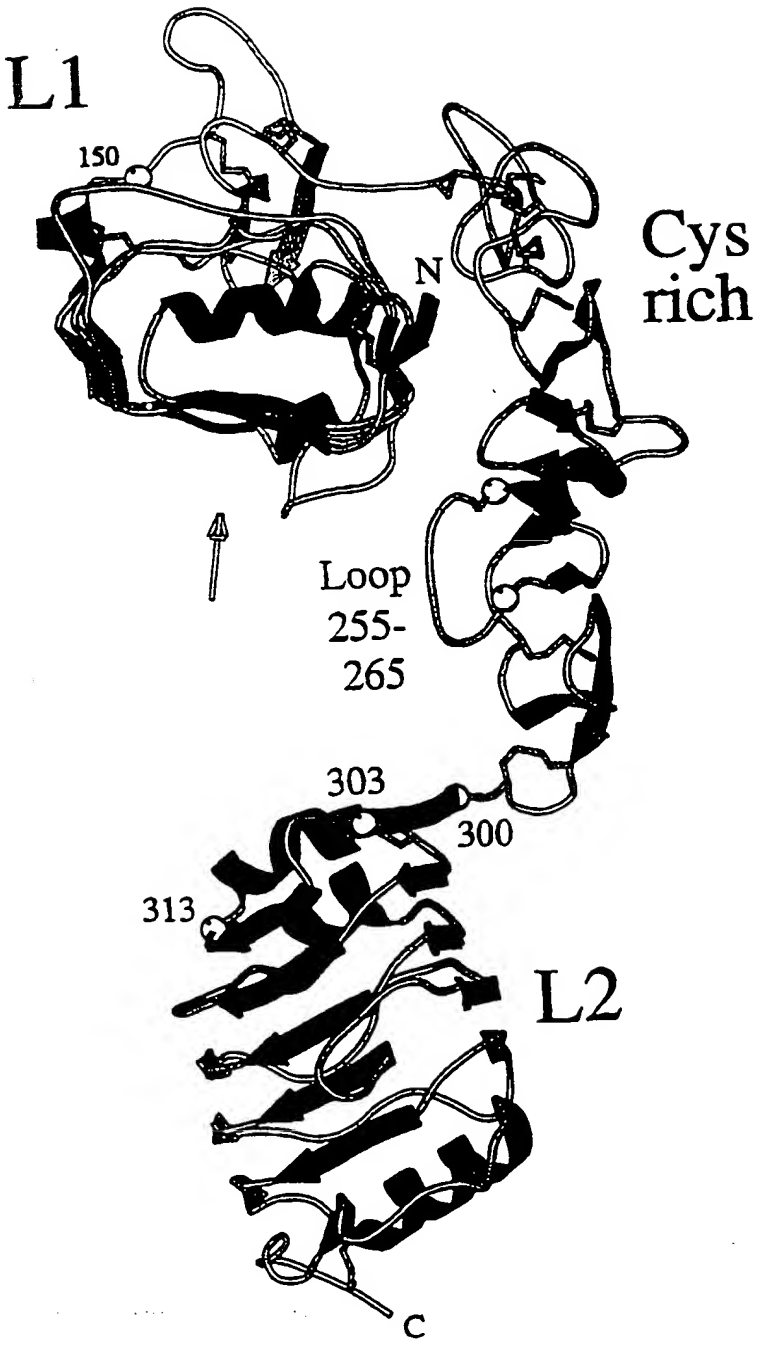
.4
.3
.2
.1
0.0
Conductivity mS/cm
1
2
3
4
0
40
80
120
160
200
Elution Volume (ml)
(b)
1 2 3 4
70 -
60 -
50 -
(c)
2

Figure 4



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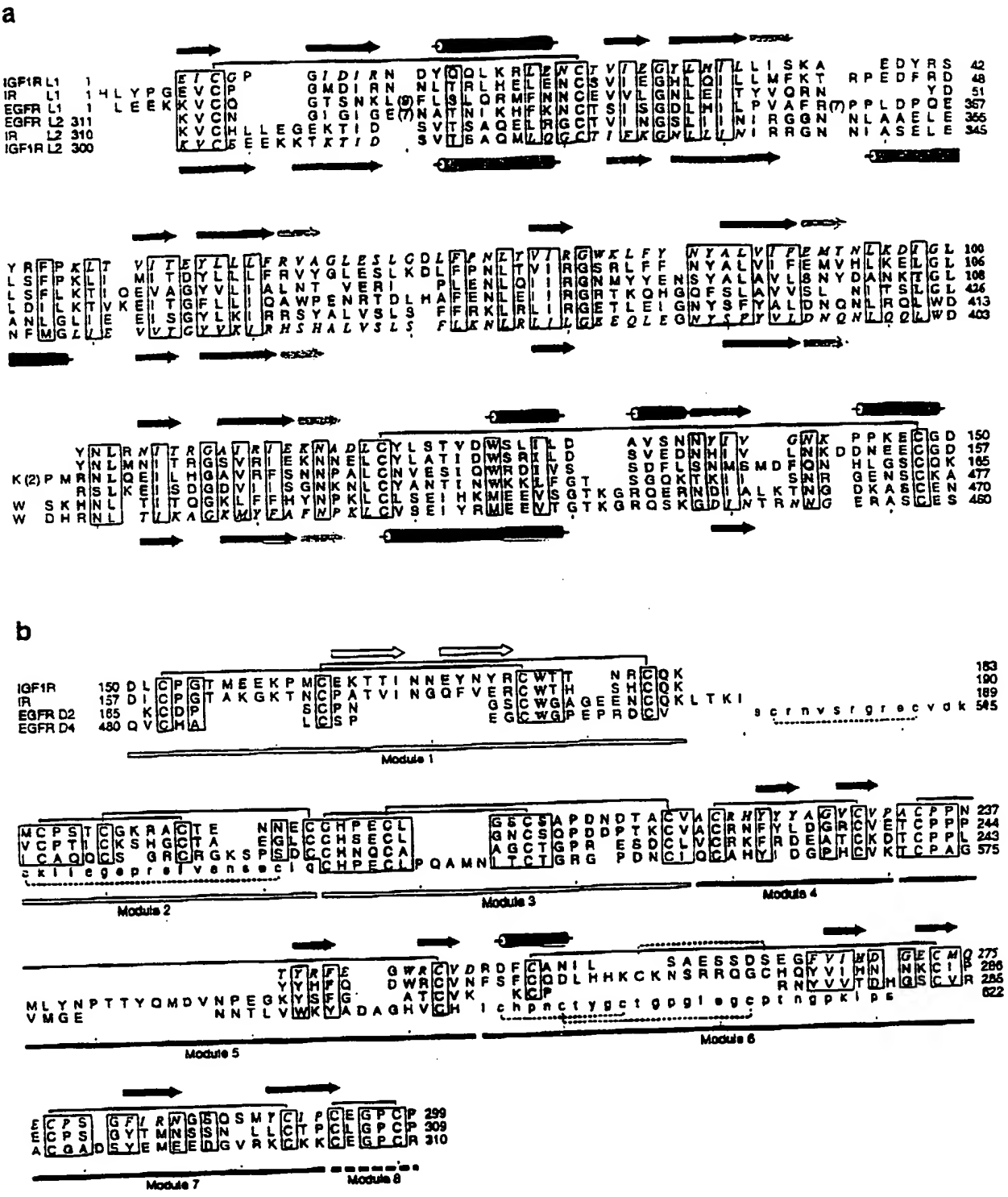
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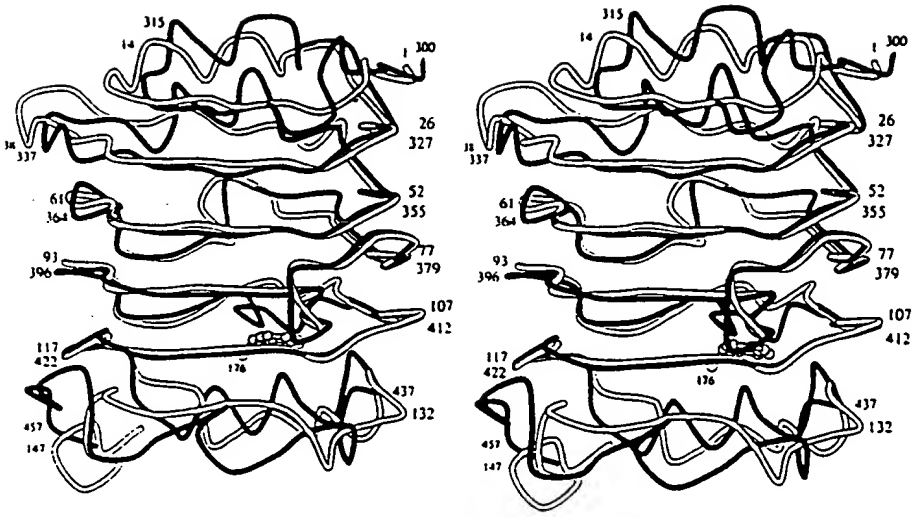
IGF1R L1
IR L1
EGFR L1
EGFR L2
IR L2
IGF1R L2
b
IGF1R
IR
EGFR D2
EGFR D4
Module 1
Module 2
Module 3
Module 4
Module 5
Module 6
Module 7
Module 8

Figure 6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457
147
315
14
1
300
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Figure 7

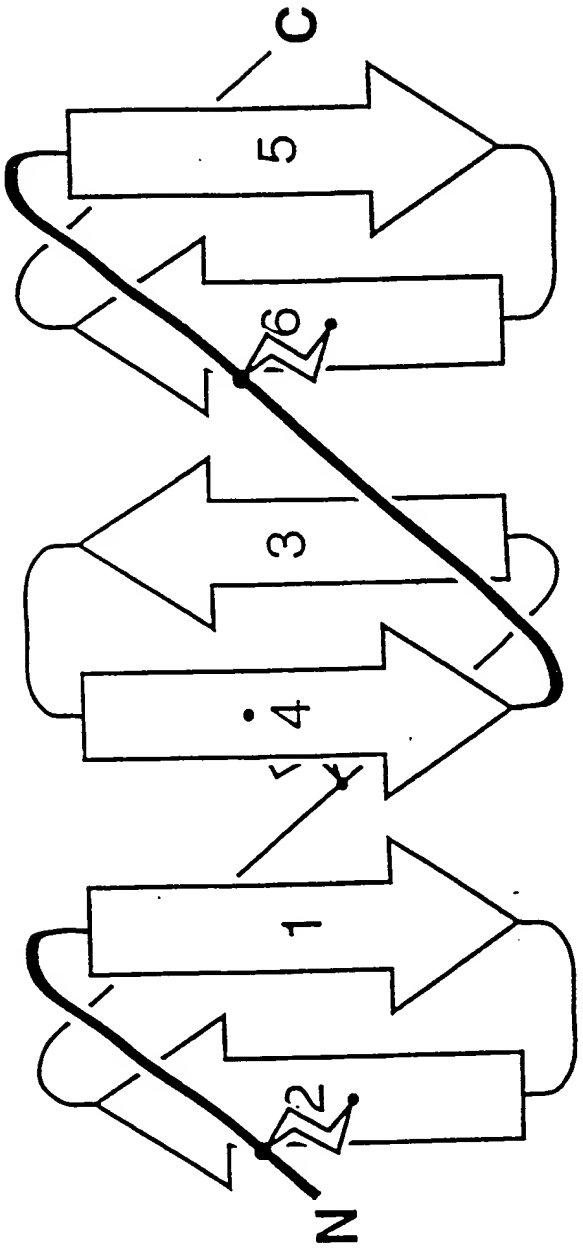

Figure 8

Figure 9: Sequence Alignment of hIGF-1R. hIR and hIRR ectodomains.

Derived by use of the PileUp program in the software package of the Genetics Computer Group, 575 Science Drive, Madison, Wisconsin, USA.

```
Symbol Comparison table: GenRunData:PileUpPep.Cmp  CompCheCk: 1254

                GapWeight: 3.0
          GapLengthWeight: 0.1

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Name: Hir             Len:   972  CheCk: 2986  Weight:  1.00
Name: Hirr            Len:   972  CheCk: 9819  Weight:  1.00

                *                       *
Higflr  .....EICGP GIDIRNDYQQ LKRLENCTVI EGYLHILLIS K..AEDYRSY 43
  Hir   HLYPGEVC.P GMDIRNNLTR LHELENCSVI EGHLQILLMF KTRPEDFRDL 49
 Hirr   ....MNVC.P SLDIRSEVAE LRQLENCSVV EGHLQILLMF TATGEDFRGL 45

Higflr  RFPKLTVITE YLLLFRVAGL ESLGDLFPNL TVIRGWKLFY NYALVIFEMT 93
  Hir   SFPKLIMITD YLLLFRVYGL ESLKDLFPNL TVIRGSRLFF NYALVIFEMV 99
 Hirr   SFPRLTQVTD YLLLFRVYGL ESLRDLFPNL AVIRGTRLFL GYALVIFEMP 95

                                        *
Higflr  NLKDIGLYNL RNITRGAIRI EKNADLCYLS TVDWSLILDA VSNNYIVGNK 143
  Hir   HLKELGLYNL MNITRGSVRI EKNNELCYLA TIDWSRILDS VEDNYIVLNK 149
 Hirr   HLRDVALPAL GAVLRGAVRV EKNQELCHLS TIDWGLLQPA PGANHIVGNK 145

            *  *                *                 *    *    *  *
Higflr  PPK.ECGDLC PGTMEEKPM. CEKTTINNEY NYRCWTTNRC QKMCPSTCGK 191
  Hir   DDNEECGDIC PGTAKGKTN. CPATVINGQF VERCWTHSHC QKVCPTICKS 198
 Hirr   LG.EECADVC PGVLGAAGEP CAKTTFSGHT DYRCWTSSHC QRVCPCPHG. 193

             *     **    *   *          *  *          *    *
Higflr  RACTENNECC HPECLGSCSA PDNDTACVAC RHYYYAGVCV PACPPNTYRF 241
  Hir   HGCTAEGLCC HSECLGNCSQ PDDPTKCVAC RNFYLDGRCV ETCPPPYYHF 248
 Hirr   MACTARGECC HTECLGGCSQ PEDPRACVAC RHLYFQGACL WACPPGTYQY 243

             *      *      *---------*          *    *
Higflr  EGWRCVDRDF CANILSAES. ...SDSEGFV IHDGECMQEC PSGFIRNGSQ 287
  Hir   QDWRCVNFSF CQDLHHKCKN SRRQGCHQYV IHNNKCIPEC PSGYTMNSSN 298
 Hirr   ESWRCVTAER CASLHSVPG. ....RASTFG IHQGSCLAQC PSGFTRNSS. 287

             *  *    *   *                    *
Higflr  SMYCIPCEGP CPKVCEEEKK TKTIDSVTSA QMLQGCTIFK GNLLINIRRG 337
  Hir   .LLCTPCLGP CPKVCHLLEG EKTIDSVTSA QELRGCTVIN GSLIINIRGG 347
 Hirr   SIFCHKCEGL CPKECKV..G TKTIDSIQAA QDLVGCTHVE GSLILNLRQG 335

Higflr  NNIASELENF MGLIEVVTGY VKIRHSHALV SLSFLKNLRL ILGEEQLEGN  387
  Hir   NNLAAELEAN LGLIEEISGY LKIRRSYALV SLSFFRKLRL IRGETLEIGN  397
 Hirr   YNLEPQLQHS LGLVETITGF LKIKHSFALV SLGFFKNLKL IRGDAMVDGN  385

                                                    *
Higflr  YSFYVLDNQN LQQLWDWDHR NLTIKAGKMY FAFNPKLCVS EIYRMEEVTG  437
  Hir   YSFYALDNQN LRQLWDWSKH NLTITQGKLF FHYNPKLCLS EIHKMEEVSG  447
 Hirr   YTLYVLDNQN LQQLGSWVAA GLTIPVGKIY FAFNPRLCLE HIYRLEEVTG  435
```

```
                                    *     !End of 1-462 fragment
Higflr  TKGRQSKGDI NTRNNGERAS CESDV  LHFTS TTTSKNRIII TWHRYRPPDY  487
   Hir  TKGRQERNDI ALKTNGDQAS CENEL  LKFSY IRTSFDKILL RWEPYWPPDF  497
  Hirr  TRGRQNKAEI NPRTNGDRAA CQTRT  LRFVS NVTEADRILL RWERYEPLEA  485
*
Higflr  RDLISFTVYY KEAPFKNVTE YDGQDACGSN SWNMVDVDLP .....PNKDV  532
   Hir  RDLLGFMLFY KEAPYQNVTE FDGQDACGSN SWTVVDIDPP LRSNDPKSQN  547
  Hirr  RDLLSFIVYY KESPFQNATE HVGPDACGTQ SWNLLDVELP L.....SRTQ  530


Higflr  EPGILLHGLK PWTQYAVYVK AVTLTMVEND HIRGAKSEIL YIRTNASVPS  582
   Hir  HPGWLMRGLK PWTQYAIFVK TL.VTFSDER RTYGAKSDII YVQTDATNPS  596
  Hirr  EPGVTLASLK PWTQYAVFVR AITLTTEEDS PHQGAQSPIV YLRTLPAAPT  580


Higflr  IPLDVLSASN SSSQLIVKWN PPSLPNGNLS YYIVRWQRQP QDGYLYRHNY  632
   Hir  VPLDPISVSN SSSQIILKWK PPSDPNGNIT HYLVFWERQA EDSELFELDY  646
  Hirr  VPQDVISTSN SSSHLLVRWK PPTQRNGNLT YYLVLWQRLA EDGDLYLNDY  630

        *                                   *   ** **  *
Higflr  CSKD.KIPIR KYADGTIDIE EVTENPKTEV CGGEKGPCCA C...PKTEAE  678
   Hir  CLKGLKLPSR TWS.PPFESE DSQKHNQSE. YEDSAGECCS C...PKTDSQ  691
  Hirr  CHRGLRLPTS N.NDPRFDGE DGDPEAEME. .....SDCCP CQHPPPGQVL  673

                                    α------->&lt;------β
Higflr  KQAEKEEAEY RKVFENFLHN SIFVPRPERK RRDVMQVANT TMSSRSRNTT  728
   Hir  ILKELEESSF RKTFEDYLHN VVFVPRPSRK RRSLGDVGNV TVAVP...TV  738
  Hirr  PPLEAQEASF QKKFENFLHN AITIPISPWK VTSINKSPQR D.SGRHRRAA  722

                                                             *
Higflr  AA..DTYNIT DPEELETEYP FFESRVDNKE RTVISNLRPF TLYRIDIHSC 776
   Hir  AAFPNTSSTS VPTSPEEHRP F..EKVVNKE SLVISGLRHF TGYRIELQAC 786
  Hirr  GPLRLGGNSS DFEIQEDKVP ........RE RAVLSGLRHF TEYRIDIHAC 764

             *
Higflr  NHEAEKLGCS ASNFVFARTM PAEGADDIPG PVTWEPRPEN SIFLKWPEPE 826
   Hir  NQDTPEERCS VAAYVSARTM PEAKADDIVG PVTHEIFENN VVHLMWQEPK 836
  Hirr  NHAAHTVGCS AATFVFARTM PHREADGIPG KVAWEASSKN SVLLRWLEPP 814

                                    *           *
Higflr  NPNGLILMYE IKYGS.QVED QRECVSRQEY RKYGGAKLNR LNPGNYTARI 875
   Hir  EPNGLIVLYE VSYRRYGDEE LHLCVSRKHF ALERGCRLRG LSPGNYSVRI 886
  Hirr  DPNGLILKYE IKYRRLGEEA TVLCVSRLRY AKFGGVHLAL LPPGNYSARV 864


Higflr  QATSLSGNGS WTDPVFFYVQ AKTGYENFIH L                     906
   Hir  RATSLAGNGS WTEPTYFYVT DYLDVPSNIA K                     917
  Hirr  RATSLAGNGS WTDSVAFYIL GPEEEDAGGL H                     895
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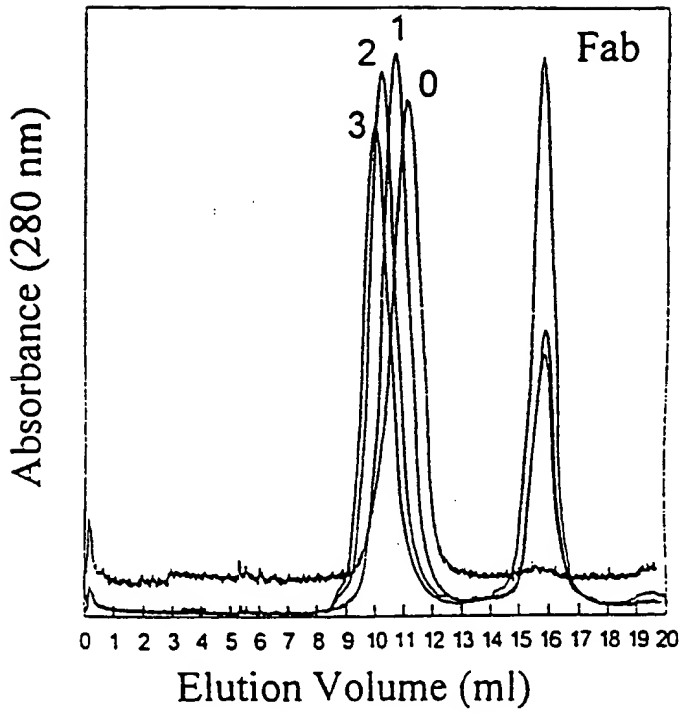
Absorbance (280 nm)
1
2
0
3
Fab
0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20
Elution Volume (ml)

Figure 10

Schematic interpretations of EM images			
Sample	Projection along: y axis	z axis	x axis
hIR			
hIR/ 83-7			
hIR/ 83-14			
hIR/ 18-44/83-14			
hIR/ 83-7/18-44			
hIR/ 83-7/83-14			

Figure 11

INTERNATIONAL SEARCH REPORT

International application No.
PCT/AU 98/00998

A. CLASSIFICATION OF SUBJECT MATTER

Int Cl[6]: C07K 14/705, 14/71; G06F 17/50, 19/00, 159:00

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
STN CAS-ON-LINE: keywords
MEDLINE :keywords

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 90/00562 (DEMEYTS) 25 January 1990 See whole document	1-33
P,X	Protein Science, 1997, no. 6, pages 2663-2666 Mckern, NM et al, "Crystallization of the first 3 domains of the human idsulin-lila growth factor -1 receptor See whole document	1-33

[X] Further documents are listed in the continuation of Box C

[X] See patent family annex

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"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

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Date of the actual completion of the international search	Date of mailing of the international search report
12 January 1999	28 JAN 1999
Name and mailing address of the ISA/AU AUSTRALIAN PATENT OFFICE PO BOX 200 WODEN ACT 2606 AUSTRALIA Facsimile No.: (02) 6285 3929	Authorized officer **OI LEE CHAI** Telephone No.: (02) 6283 2482

INTERNATIONAL SEARCH REPORT

International application No.
PCT/AU 98/00998

C (Continuation). **DOCUMENTS CONSIDERED TO BE RELEVANT**

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P,X	Nature, vol 394, published 23 July 1998, pages 395-399, Garrett TPJ et al, "Crystal Structure of the first 3 domains of the type -1 insulin-litu growth factor-1 receptor See whole document	1-33

INTERNATIONAL SEARCH REPORT

Information on patent family members

Internauonal application No
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This Annex lists the known "A" publication level patent family members relating to the patent documents cited in the above-mentioned international search report. The Australian Patent Office is in no way liable for these particulars which are merely given for the purpose of information.

Patent Document Cited in Search Report		Patent Family Member					
WO	90/00562	AU	39822/89	DE	68927854	EP	378671
		JP	3501487	US	5227466		

END OF ANNEX

CORRECTED VERSION*

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INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

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(74) Agent: F.B. RICE & CO.; 605 Darling Street, Balmain, NSW 2041 (AU).

(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

Published
With international search report.

(54) Title: METHOD OF DESIGNING AGONISTS AND ANTAGONISTS TO IGF RECEPTOR

(57) Abstract

The present invention relates to a method of designing compounds able to bind to a molecule of the insulin receptor family and to modulate the activity mediated by the receptor based on the 3–D structure coordinates of a IGF–1 receptor crystal of Figure 1.

*(Referred to in PCT Gazette No. 35/1999, Section II)

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